

Figure 1. Muscle cramping of the Cral mouse.



Cral/+

+/+

BEST AVAILABLE COPY

Figure 2. Increased ambulatory activity of Cra1 mice during the night.

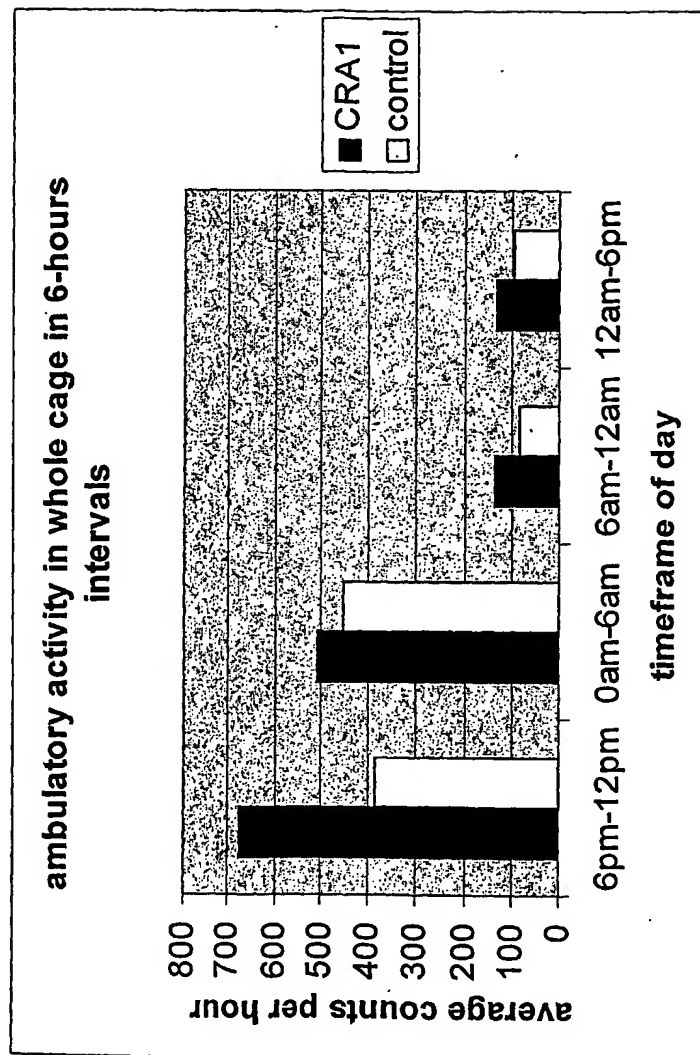
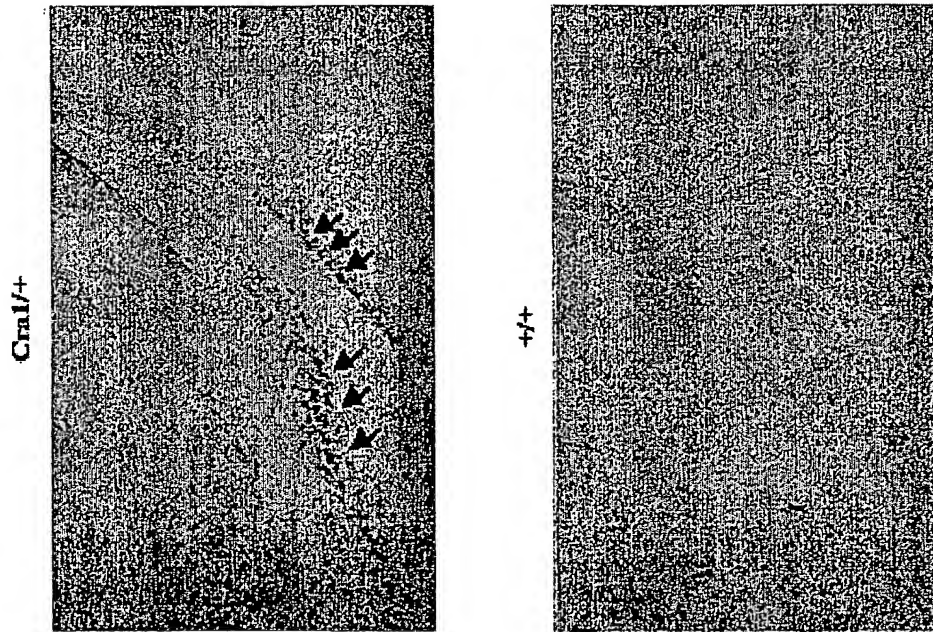


Figure 3. Reduced muscle endurance of *Cral* mice.

<u>Mouse #</u>	<u>Sex</u>	<u>Genotype</u>	<u>Latency to Fall [in seconds]</u>
1	female	+/+	810
2	male	+/+	280
3	male	+/+	845
4	female	<i>Cral</i> /+	110
5	female	<i>Cral</i> /+	15
6	female	<i>Cral</i> /+	35
7	male	<i>Cral</i> /+	14
8	male	<i>Cral</i> /+	20
9	male	<i>Cral</i> /+	20

Figure 4. Excitatory neuronal damage in the hippocampus of the *Cra1* mouse.



BEST AVAILABLE COPY

Figure 5. Neurodegeneration in the anterior horns of the spinal cord and the dorsal root ganglia of homozygous Cra1 embryos.

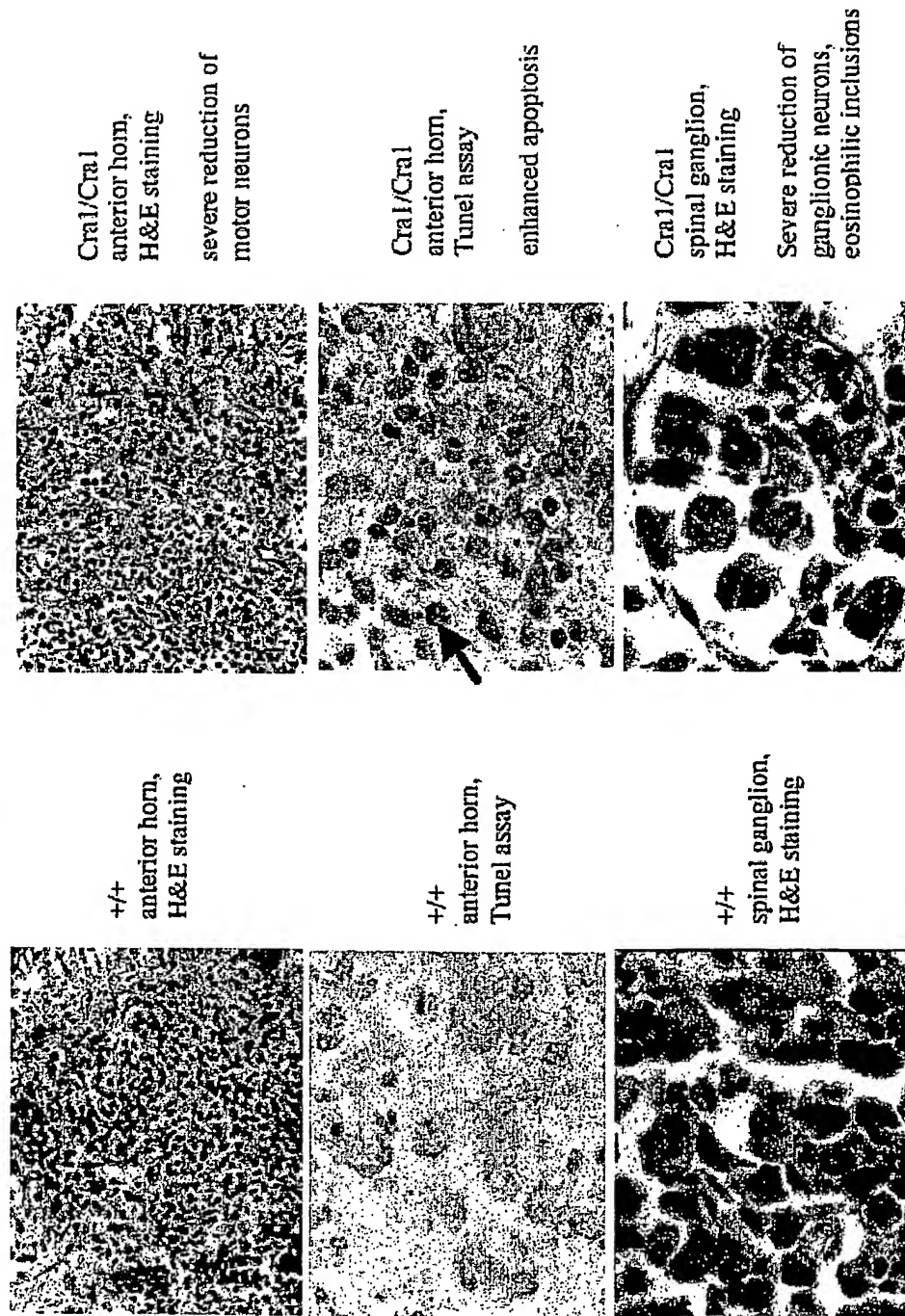
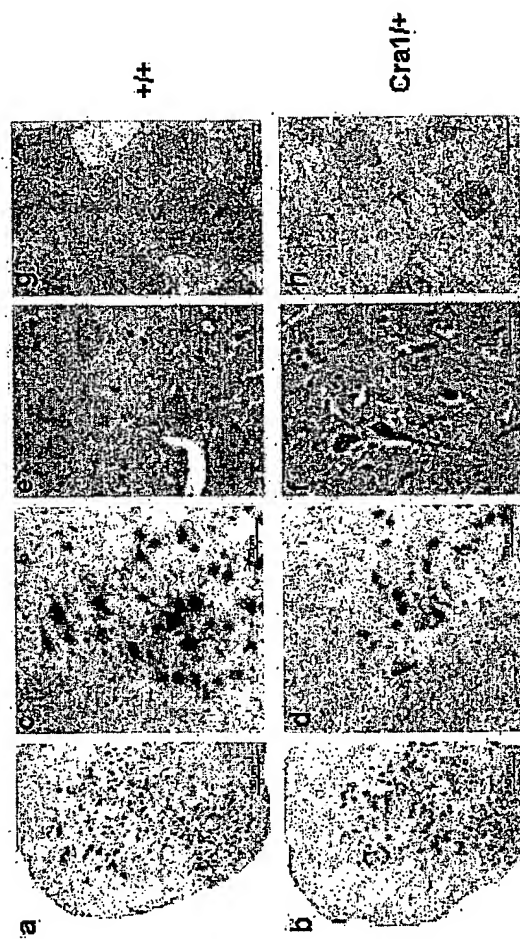


Figure 5.2: Progressive impairment of muscle function and motor coordination is associated with decreasing numbers of a-motor neurons and altered composition of muscle fibre types.

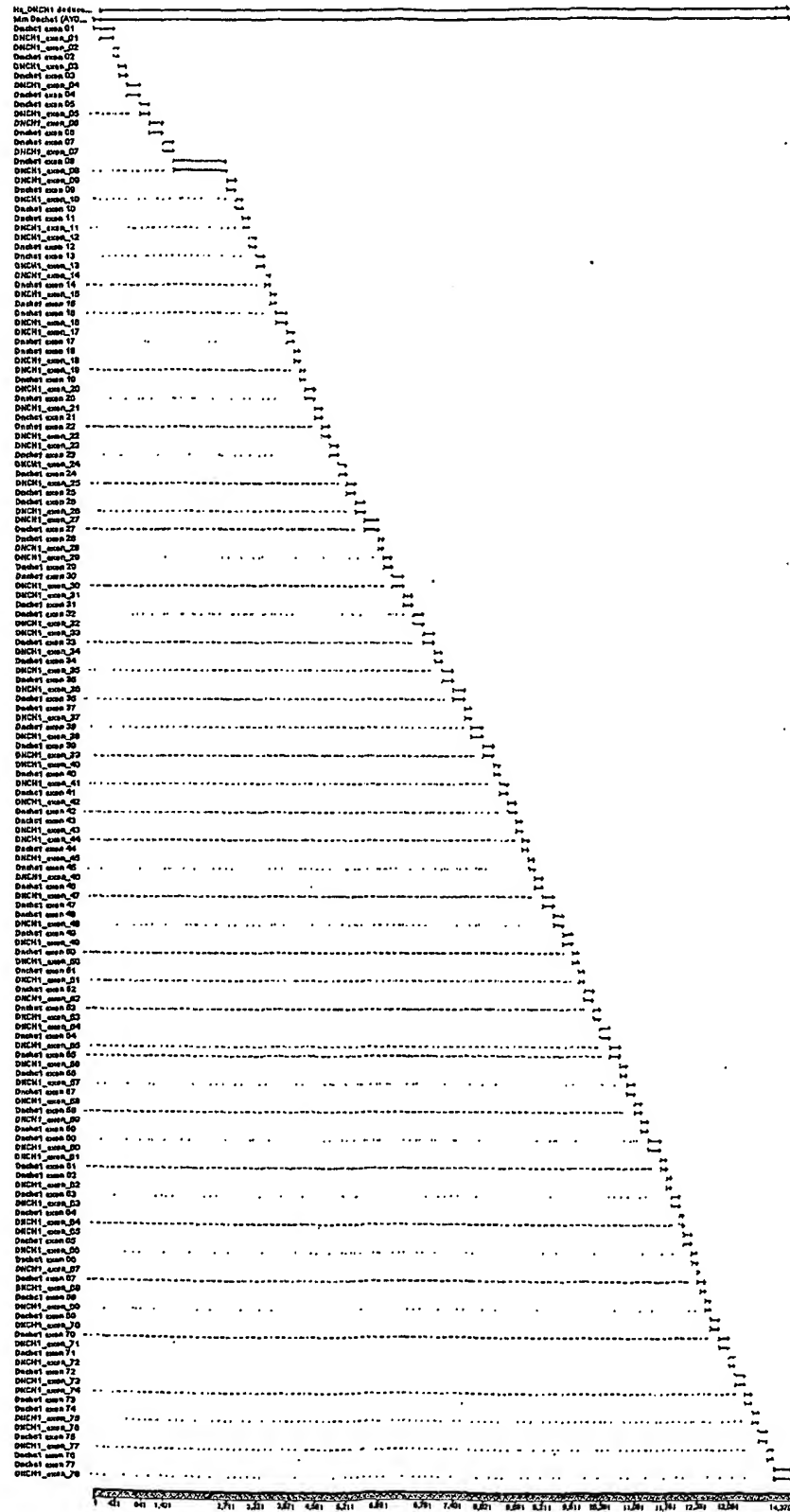


**BEST AVAILABLE COPY**

Gene symbol	Gene description:	Deregulation	Biological significance
Rasgrp2	RAS, guanyl releasing protein 2	Up	Brain-enriched guanine nucleotide exchange factor; is stimulated by calcium and diacylglycerol and activates small GTPases. (e.g. Ras); expressed in the striatal projection neurons (cf. Toki et al. 2001, J Comp Neurol 437, 398-407)
Vdac2	voltage-dependent anion channel 2	Down	Voltage dependent anion channel of the outer mitochondrial membrane; controls the permeability of outer mitochondrial membrane for anions (eg ATP); probably part of the permeability transition pore (involved in apoptosis regulation); KO mouse displays immotile sperms and infertility (experimental oligos, of the sperms) as well as deficits in long and short term synaptic plasticity, fear conditioning and spatial learning (cf. Weeber et al. 2002, J Biol Chem 277, 18891-18897).
Ttc3	tetratricopeptide repeat domain	Down	Domain on microtubulins that allows them to bind to an acceptor site on the ubiquitous hsp90 protein; some of these microtubulins by another domain (PPIase) bind to cytochrome c; the complex of the hsp90-GR (glucocorticoid receptor)-FKBP52 is targeted to the nucleus by binding of the latter to GR (cf. Harrell et al. 2002, 41, 5581-5587)
Rab6	RAB6, member RAS subfamily	Down	Rab proteins are molecular switches or timers regulating the transport of vesicles between compartments of the cell (eg golgi and ER); they impact the recruitment of dynein to the intracellular vesicles which have to be transported (cf. Smythe 2002, Mol. Cell 9, 205-206; Szebia et al 2002, Trends Mol Med 8, 23-30)
Rab2	RAB2, member RAS subfamily	Down	Rab proteins are molecular switches or timers regulating the transport of vesicles between compartments of the cell (eg golgi and ER); they impact the recruitment of dynein to the intracellular vesicles which have to be transported (cf. Smythe 2002, Mol. Cell 9, 205-206; Szebia et al 2002, Trends Mol Med 8, 23-30)
Pak3	p21 (COGMA)-activated kinase 3	Down	PAK proteins (p21 activating kinases) are downstream effectors that link Rho GTPases to the actin cytoskeleton and to MAP kinase cascades, including the c-Jun amino-terminal kinase (JNK) and p38. Recently it has been shown, that the presence of mutations in Pak3 is associated with X-linked non-specific mental retardation (Blagovenu, T. et al 2000, AM J Med Genet. 93, 294-298)
Mark3	MAP/microtubule affinity-regulating kinase 3	Down	Belongs to a family of kinases which phosphorylates microtubule-associated proteins (e.g. tau) and trigger microtubule disruption (cf. Drewes et al 1997, Cell 89, 297-308); tau is hyperphosphorylated in several neurodegenerative diseases including Alzheimers disease (cf. Schneider et al. 1999, Biochemistry 38, 3549-3558)
Kif3b	kinase family member 3b	Down	Component of the anterograde motor kinesin (Yamazaki et al 1995, J Cell Biol 130, 1387-1393)
Drg1	developmentally regulated GTP binding protein 1	Down	DRG is a developmentally regulated GTP-binding protein from the central nervous system of mouse (LI and Truett, 2000, Blochim Biophys Acta 1491, 196-204).
Cttn3	chloride channel 3	Down	Cic3 chloride channel is expressed in nervous tissue; the KO mouse displays blindness; motor coordination deficit; spontaneous hypoglossal, retinal and hippocampal degeneration; the observed phenotype seems to be due to an accumulation of the neuronal ceroid lipofuscin
Bcan	brevican	Down	Brevican is an extracellular matrix molecule (proteoglycan) which is overexpressed in human gliomas (Gawinski et al 1996, Cancer Research 56, 2293-2298). It seems to inhibit neurite outgrowth thereby contributing to axon guidance in development and regenerative processes (cf. Deller et al. 2001, Restor Neurol Neurosci 19, 159-167)

**BEST AVAILABLE COPY**

Figure 7. Exon Structure Comparison between the Human DNCH1 and the Mouse Dnchc1 Genes.



BEST AVAILABLE COPY



Figure 8. Comparison of mouse and human dynein heavy chain 1 exon numbers and exon lengths.

Exon No.	Mm Dnchc1 (bp)	Hs DNCH1 (bp)	Exon No.	Mm Dnchc1 (bp)	Hs DNCH1 (bp)
1	250	256	40	122	122
2	88	88	41	166	166
3	174	174	42	164	164
4	256	256	43	130	130
5	187	187	44	134	134
6	272	272	45	115	115
7	228	228	46	162	162
8	1078	1078	47	215	215
9	180	180	48	205	205
10	150	150	49	174	174
11	147	147	50	120	120
12	141	141	51	121	121
13	177	177	52	196	196
14	111	111	53	118	118
15	120	120	54	216	216
16	240	240	55	213	213
17	156	156	56	128	128
18	114	114	57	154	154
19	111	111	58	147	147
20	210	210	59	151	151
21	147	147	60	254	254
22	167	167	61	135	135
23	174	174	62	95	95
24	166	166	63	175	175
25	189	189	64	76	76
26	195	195	65	161	161
27	283	283	66	112	112
28	101	101	67	185	61
29	160	160	68	114	124
30	244	244	69	171	114
31	184	184	70	218	171
32	213	213	71	104	218
33	239	239	72	212	104
34	157	157	73	154	212
35	228	228	74	143	154
36	231	231	75	169	143
37	141	141	76	128	169
38	234	234	77	129	128
39	207	207	78		129

Figure 9. Amino Acid Alignment of Human DNCH1 and Mouse Dnchc1 Proteins.

Hs_DNCH1	1	KSEPGGGGEGDSAGLEVSQNVADVSLQKHRLKLVPLLEDGGAPAALEAEAEKSALEQMRKFLSDPQVHTVIVVERSTLKEDVGDGEGEEKEEFTS
Mm_Dnchc1	1	VSEPGGG...EDGSAGLEVSQNVADVA/LQKHRLKLVPLLEDGGAPAALEAEAEKSALEQMRKFLSDPQVHTVIVVERSTLKEDVGDGEGEEKEEFTS
Hs_DNCH1	101	YMINLDIYGVKSNLSLAFIRKTPVLDADKPVSQSLRVLTLSSEDSPYETLHSTFISNAVAPFFKSYIRESKADRDGDKMAPSVVEKKTAELEMGILLHLQQNI
Mm_Dnchc1	99	YMINLDIHYGVKSNLSLAFIRKTPVLDADKPVSQSLRVLTLSSEDSPYETLHSTFISNAVAPFFKSYIRESKADRDGDKMAPSVVEKKTAELEMGILLHLQQNI
Hs_DNCH1	201	EIPEISLPIHPIITWAKQCYERGEKPKVTDGDKVEDPTEINQOSGVNRWIREIQKVTIKIDRDPASGTALQEI SFWILERAIYRIOEKRESPEVLLT
Mm_Dnchc1	199	EIPEISLPIHPIITWAKQCYERGEKPKVTDGDKVEDPTEINQOSGVNRWIREIQKVTIKIDRDPASGTALQEI SFWILERADYRIOEKRESPEVLLT
Hs_DNCH1	301	LDLLKIGKRPHATVSFDTDTG/KOALETVNDYNPLMKDPLNDLLSATLQALVAIFTHLRKIRNTKYPIORALRLVEAISRDLSSQLLKVLGTRK
Mm_Dnchc1	299	LDLLKIGKRPHATVSFDTDTG/KOALETVNDYNPLMKDPLNDLLSATLQALVAIFTHLRKIRNTKYPIORALRLVEAISRDLSSQLLKVLGTRK
Hs_DNCH1	401	LHVAYEEFEKVMVACFEVFQTDDEYEKQLVLRDIIVKRKEENLWVRINPAHRKLOARLDQHRKERRQHEQOLRAVIVRLRQVTVAVAAQNGGEMP
Mm_Dnchc1	399	LHVAYEEFEKVMVACFEVFQTDDEYEKQLVLRDIIVKRKEENLWVRINPAHRKLOARLDQHRKERRQHEQOLRAVIVRLRQVTVAVAAQNGGEMP
Hs_DNCH1	501	EPQDMKVAEVLFDAAADANLIEEVNLAIVENKREVDGLDVSKEGTEAEAKMKRYDERIDRVETRI/TARLDQ/LGTAKNANEMERIFSRFWALFVRPHIRGA
Mm_Dnchc1	499	EPQDMKVAEVLFDAAADANLIEEVNLAIVENKREVDGLDVSKEGTEAEAKMKRYDERIDRVETRI/TARLDQ/LGTAKNANEMERIFSRFWALFVRPHIRGA
Hs_DNCH1	601	IREYOTQ/LIQRVKDDIESLHDKFKVQVPOSQACNMSHVRDLPVSGSIIWAKQIDROLTA/YMKRVEDVLGKRWENHVEGQKLKQDGDSPRMKINTQEIIFD
Mm_Dnchc1	599	IREYOTQ/LIQRVKDDIESLHDKFKVQVPOSQACNMSHVRDLPVSGSIIWAKQIDROLTA/YMKRVEDVLGKRWENHVEGQKLKQDGDSPRMKINTQEIIFD
Hs_DNCH1	701	QWARKVQORNILGVSGRIFTTIESA/RVGRGTGNVLKLVNLFPEITLSKEVRNKLWLGFRVPIA/VNKAHQANQLYPPFAISLIESVTVERTCEKVEERNVT
Mm_Dnchc1	699	QWARKVQORNILGVSGRIFTTIESA/RVGRGTGNVLKLVNLFPEITLSKEVRNKLWLGFRVPIA/VNKAHQANQLYPPFAISLIESVTVERTCEKVEERNVT
Hs_DNCH1	801	ISLLVAGLKKREVOALIAEGTALVWESYKLDIPYQRLAETVFNFOEKVDLLTIIEEKIDLEVRSLTCTCHYDHTTSEILNVRVQKAVDDLLRLHSYSLPIRV
Mm_Dnchc1	799	ISLLVAGLKKREVOALIAEGTALVWESYKLDIPYQRLAETVFNFOEKVDLLTIIEEKIDLEVRSLTCTCHYDHTTSEILNVRVQKAVDDLLRLHSYSLPIRV
Hs_DNCH1	901	NKLDMEIERILGVRLQAGLRATQVLLGQAEKAEVDMDDTAPQVSHKPGGEPKIKNVVHELRI/TNOVIYLNPPITEECRYKLYQEMFAWKVWVLSLPRIQ
Mm_Dnchc1	899	NKLDMEIERILGVRLQAGLRATQVLLGQAEKAEVDMDDTAPQVSHKPGGEPKIKNVVHELRI/TNOVIYLNPPITEECRYKLYQEMFAWKVWVLSLPRIQ
Hs_DNCH1	1001	SQRQVGVHYVELTEEEKPYRNALTRMPDGPVVALEESYSANVGI/VHEVEQYKVM/LQYQCLMDQAEHIYNNRIGEDLNKQALLVQIRKARGTFDNAETKK
Mm_Dnchc1	999	SQRQVGVHYVELTEEEKPYRNALTRMPDGPVVALEESYSANVGI/VHEVEQYKVM/LQYQCLMDQAEHIYNNRIGEDLNKQALLVQIRKARGTFDNAETKK
Hs_DNCH1	1101	EFGPVVLDYGVKQSVKVLKYDSHHKEVLSKFGQMLGNNMTFFHSQISKSROELQHSVDTAFTFYVQS/LKRIKIOFEKQVLYRNGQRLLEKO
Mm_Dnchc1	1099	EFGPVVLDYGVKQSVKVLKYDSHHKEVLSKFGQMLGNNMTFFHSQISKSROELQHSVDTAFTFYVQS/LKRIKIOFEKQVLYRNGQRLLEKO
Hs_DNCH1	1201	RFQPPPSWLYTDNI/EGEWGAFNDIMRRKDSAI/QQVANLQMKI/VQEDRAVESRTD/LITDHEKTKPVTGNLRPEEALQALTIYEGKFGRLKDDREKCAKA
Mm_Dnchc1	1199	RFQPPPSWLYTDNI/EGEWGAFNDIMRRKDSAI/QQVANLQMKI/VQEDRAVESRTD/LITDHEKTKPVTGNLRPEEALQALTIYEGKFGRLKDDREKCAKA

BEST AVAILABLE COPY

(Figure 9 continued)

Hs\_DNCH1 1301 KALELTDGLSGSERVQVALEELQDLKGVSELSKWEQIDQMKQEPWVSQPRKLRQNLDELINQKLSFARLRQVASYEFVORLLKGYMKINMLV  
 Mm\_Dnchc1 1299 KALELTDGLSGSERVQVALEELQDLKGVSELSKWEQIDQMKQEPWVSQPRKLRQNLDELINQKLSFARLRQVASYEFVORLLKGYMKINMLV  
 Hs\_DNCH1 1401 IEKLSALKDRHWKQKMLKRHHVNVVSEITLQGIQMDVDLQKNEATIKVDVLLAQAGWALEEFKQIREVNTVYELDLVNTQNKCRLLIRGWDDLEFNKVKKEH  
 Mm\_Dnchc1 1399 IEKLSALKDRHWKQKMLKRHHVNVVSEITLQGIQMDVDLQKNEATIKVDVLLAQAGWALEEFKQIREVNTVYELDLVNTQNKCRLLIRGWDDLEFNKVKKEH  
 Hs\_DNCH1 1501 INSVSAMKLSPPYKVVFEEDALSMEDKLRIMAFDWIIVQRRWVLEGIFTGSAADIKHLLPVETQFOSISTEFLALMKKVSPLVMDVLNLQGVQORS  
 Mm\_Dnchc1 1499 INSVSAMKLSPPYKVVFEEDALSMEDKLRIMAFDWIIVQRRWVLEGIFTGSAADIKHLLPVETQFOSISTEFLALMKKVSPLVMDVLNLQGVQORS  
 Hs\_DNCH1 1601 LERLADLLGKIQKALGEYLERESSPPRFYFVGDEDLLEIIGNSKIVAKLQKHFKAFFAGVASSIILINEONSVVLGIFSSREGEVMEFKTPVSIITEHPKINE  
 Mm\_Dnchc1 1599 LERLADLLGKIQKALGEYLERESSPPRFYFVGDEDLLEIIGNSKIVAKLQKHFKAFFAGVASSIILINEONSVVLGIFSSREGEVMEFKTPVSIITEHPKINE  
 Hs\_DNCH1 1701 MTLVKEKMRVTLAKLLAESVTEVEIFGKATSIDENTVYITWIDKYQAQVWLSAQAMSENVEMALSNGGGGVYPLASVLSNVVETLVNLADSVLNEQ  
 Mm\_Dnchc1 1699 MTLVKEKMRVTLAKLLAESVTEVEIFGKATSIDENTVYITWIDKYQAQVWLSAQAMSENVEMALSNGGGGVYPLASVLSNVVETLVNLADSVLNEQ  
 Hs\_DNCH1 1801 PPLRRRKLLEHLITELVHORDVTRSLIKSKI DNKAKSEFMSQHRFEYDPKQTDVLOQLSIQMANAKFNFGFEYIGVQDKLVQVTELTDRCYLTMTQALEARL  
 Mm\_Dnchc1 1799 PPLRRRKLLEHLITELVHORDVTRSLIKSKI DNKAKSEFMSQHRFEYDPKQTDVLOQLSIQMANAKFNFGFEYIGVQDKLVQVTELTDRCYLTMTQALEARL  
 Hs\_DNCH1 1901 SCSPGPGVAGTGTESVKALGHQGRFVLFVNCDETFDQAGRIIFVGLCQAGWGTDEFNRLERMLSAVSQVQCIQBALREHSNPNVDKTSAPITCE  
 Mm\_Dnchc1 1899 SCSPGPGVAGTGTESVKALGHQGRFVLFVNCDETFDQAGRIIFVGLCQAGWGTDEFNRLERMLSAVSQVQCIQBALREHSNPNVDKTSAPITCE  
 Hs\_DNCH1 2001 LANKQVKSPPONALFITMNPYAGKSNLPDNLKLFRLSIAMTKPQRLTAQVMLYSQGRFTRAEVLANKIUPPFKLCDEQLSSQSHYDFGRLAKLSVLVSA  
 Mm\_Dnchc1 1999 LANKQVKSPPONALFITMNPYAGKSNLPDNLKLFRLSIAMTKPQRLTAQVMLYSQGRFTRAEVLANKIUPPFKLCDEQLSSQSHYDFGRLAKLSVLVSA  
 Hs\_DNCH1 2101 GNVKREIQTIKREKEGEAVDEGEIAENLPEQELLIQSVCTETVPKLVAEADIPLLSLSDVPFGVQYHRGEMTALREELKKVCQEMLYTYGDGEVNG  
 Mm\_Dnchc1 2099 GNVKREIQTIKREKEGEAVDEGEIAENLPEQELLIQSVCTETVPKLVAEADIPLLSLSDVPFGVQYHRGEMTALREELKKVCQEMLYTYGDGEVNG  
 Hs\_DNCH1 2201 GNVKREIQTIKREKEGEAVDEGEIAENLPEQELLIQSVCTETVPKLVAEADIPLLSLSDVPFGVQYHRGEMTALREELKKVCQEMLYTYGDGEVNG  
 Mm\_Dnchc1 2199 GNVKREIQTIKREKEGEAVDEGEIAENLPEQELLIQSVCTETVPKLVAEADIPLLSLSDVPFGVQYHRGEMTALREELKKVCQEMLYTYGDGEVNG  
 Hs\_DNCH1 2301 IVFGDGDVPEWVENLNSVLDNKLITLNGERLSLPPNVRIMFEVQDLKYATLATVSRCCGMWFSEDLVSTDMIENNFLARLSIPLDGEDEAQRNRKG  
 Mm\_Dnchc1 2299 IVFGDGDVPEWVENLNSVLDNKLITLNGERLSLPPNVRIMFEVQDLKYATLATVSRCCGMWFSEDLVSTDMIENNFLARLSIPLDGEDEAQRNRKG  
 Hs\_DNCH1 2401 KEDEGEAASPNLOIQRDAATIMQPYFTSNGLVTKALHAFQLEHIMDLTRLCIGSLFSLMHQACRNVAAQVNAHPDPFPMQIEQLERYIQRYLVYAILW  
 Mm\_Dnchc1 2399 KEDEGEAASPNLOIQRDAATIMQPYFTSNGLVTKALHAFQLEHIMDLTRLCIGSLFSLMHQACRNVAAQVNAHPDPFPMQIEQLERYIQRYLVYAILW  
 Hs\_DNCH1 2501 SLSDSRKMKRAELGEYIRRTITVPLTPAPNPIIDYEVSISSGWSPPQAKVPOLEVETHKVAAPDVVVPITLDVWRHEALLYTWLAHEKPLVLCGPPGSG  
 Mm\_Dnchc1 2499 SLSDSRKMKRAELGEYIRRTITVPLTPAPNPIIDYEVSISSGWSPPQAKVPOLEVETHKVAAPDVVVPITLDVWRHEALLYTWLAHEKPLVLCGPPGSG  
 Hs\_DNCH1 2601 KTWTLFSAALRALPDMEVUGLNFSSATTEPELLKTEDHYCEYRRTPNGVVLAPVQIGKWLVLFCDEINLPMDDKYGTQVVISFIROMVEHGAFRTSDQW  
 Mm\_Dnchc1 2599 KTWTLFSAALRALPDMEVUGLNFSSATTEPELLKTEDHYCEYRRTPNGVVLAPVQIGKWLVLFCDEINLPMDDKYGTQVVISFIROMVEHGAFRTSDQW  
 Hs\_DNCH1 2701 VKLERIQFVGACNPPDGRKPLSHRFLRHVPVYVDYVPGASITQIYGTENRAMRLIPLSIRTYAEPLTAMVEFYTMSQERFTQDQPHYIYSPREMT  
 Mm\_Dnchc1 2699 VKLERIQFVGACNPPDGRKPLSHRFLRHVPVYVDYVPGASITQIYGTENRAMRLIPLSIRTYAEPLTAMVEFYTMSQERFTQDQPHYIYSPREMT  
 Hs\_DNCH1 2801 RAVRGIFEARPLETLPVEGLIRIWAHEALRALFODRLVEDEERRWTDENIOWALKHFPNIDHEKAMSRPILYSNMLSKDYIPVDOEELRDYVKARLKV  
 Mm\_Dnchc1 2799 RAVRGIFEARPLETLPVEGLIRIWAHEALRALFODRLVEDEERRWTDENIOWALKHFPNIDHEKAMSRPILYSNMLSKDYIPVDOEELRDYVKARLKV

(Figure 9 continued)

BEST AVAILABLE COPY

Hs\_DNCH1 2901 YEEBDDVPLVLFNEVLDHVLRI DRI FRQPOGHLLIIGVSGAGTTLTSGFVAMNGLSVYQIKVHRKTYGDEDEDLRTVLRSGCKNEKIA FIMDES NVL  
 Mm\_Dnchc1 2899 YEEBDDVPLVLFNEVLDHVLRI DRI FRQPOGHLLIIGVSGAGTTLTSGFVAMNGLSVYQIKVHRKTYGDEDEDLRTVLRSGCKNEKIA FIMDES NVL  
 Hs\_DNCH1 3001 DSGFLERANWTL LANGEVPG LPEGDEYATLTQCKEGAKQEGMLDSHBEYKWTQSQUIRNLHV VFTWNPSSSEGLKDRATSPALFNRCVLNFWGDMSTE  
 Mm\_Dnchc1 2999 DSGFLERANWTL LANGEVPG LPEGDEYATLTQCKEGAKQEGMLDSHBEYKWTQSQUIRNLHV VFTWNPSSSEGLKDRATSPALFNRCVLNFWGDMSTE  
 Hs\_DNCH1 3101 ALXOVGKFTSKMOLEKPNXIVPDYMPVVDKLPQPPHREAI VNSCVFVHQTILQANARLAKRGGRMTATPRHYLDFTINHYANLFTHEKRSSELEEQMH  
 Mm\_Dnchc1 3099 ALXOVGKFTSKMOLEKPNXIVPDYMPVVDKLPQPPHREAI VNSCVFVHQTILQANARLAKRGGRMTATPRHYLDFTINHYANLFTHEKRSSELEEQMH  
 Hs\_DNCH1 3201 LNWGLRKIKETVDOVEELRRDLRI KSOELEVKNAANDKLKWKVDQOEAKKVMQSOETQEOHLHQOEVTADKQMSVKEDIDKVEPAVIERAONAVKSTK  
 Mm\_Dnchc1 3199 LNWGLRKIKETVDOVEELRRDLRI KSOELEVKNAANDKLKWKVDQOEAKKVMQSOETQEOHLHQOEVTADKQMSVKEDIDKVEPAVIERAONAVKSTK  
 Hs\_DNCH1 3301 KOHLVEVRSHANPPAAVKLALESTICLALGESTYDMKQI RSI IINRENTPTI VNPSSAEISDAIREKKNKVMSPSYNYEIVNRSALACGFWVWVAIAQL  
 Mm\_Dnchc1 3299 KOHLVEVRSHANPPAAVKLALESTICLALGESTYDMKQI RSI IINRENTPTI VNPSSAEISDAIREKKNKVMSPSYNYEIVNRSALACGFWVWVAIAQL  
 Hs\_DNCH1 3401 AYADMLKRVPELRNELQKLEDDAKDNQCKANEVEQNI RDLEASTARYKEEYAVLISEAQAIKADLA AVEAKVNRSTALLKLSABERWEKTSSETKQOM  
 Mm\_Dnchc1 3399 AYADMLKRVPELRNELQKLEDDAKDNQCKANEVEQNI RDLEASTARYKEEYAVLISEAQAIKADLA AVEAKVNRSTALLKLSABERWEKTSSETKQOM  
 Hs\_DNCH1 3501 STIAGDCLISAAFIAYAGYFDQOMRQNLFTWSSHLLQOANI QERTDIARTEYLSNADERLRMQASSLPADDLCTENAIMLRFRNRYPLIIDPSGOATEFI  
 Mm\_Dnchc1 3499 STIAGDCLISAAFIAYAGYFDQOMRQNLFTWSSHLLQOANI QERTDIARTEYLSNADERLRMQASSLPADDLCTENAIMLRFRNRYPLIIDPSGOATEFI  
 Hs\_DNCH1 3601 MNEYKURKI TRTSFLDDAFKKNLESALRFGNPLLVODVESYDVPVLPVNLNREVRRTGGRVLIITIGDQDIDIDSPSFVIFLSTRDPTVEFPDLC SRVTFVN  
 Mm\_Dnchc1 3599 MNEYKURKI TRTSFLDDAFKKNLESALRFGNPLLVODVESYDVPVLPVNLNREVRRTGGRVLIITIGDQDIDIDSPSFVIFLSTRDPTVEFPDLC SRVTFVN  
 Hs\_DNCH1 3701 FTWTRSSLOQCLNEVLKAEKRPDVDEKRSLLKLOGEFOLRLQLEKSLLOALNEVKGRILLDDTITITLENLAREAAEVTRKVEETDIVAQEVETVSQC  
 Mm\_Dnchc1 3699 FTWTRSSLOQCLNEVLKAEKRPDVDEKRSLLKLOGEFOLRLQLEKSLLOALNEVKGRILLDDTITITLENLAREAAEVTRKVEETDIVAQEVETVSQC  
 Hs\_DNCH1 3801 YLPLSTACSSIIYFTMESLQVHELYQVSLQOFFLDIYHNVLYENPNLKGVTDDHTQRLSII TKDLFOVAFNVRARGMLHQDHTFANILLARIKLKGTVGEBPT  
 Mm\_Dnchc1 3799 YLPLSTACSSIIYFTMESLQVHELYQVSLQOFFLDIYHNVLYENPNLKGVTDDHTQRLSII TKDLFOVAFNVRARGMLHQDHTFANILLARIKLKGTVGEBPT  
 Hs\_DNCH1 3901 YDAEFQHFIRGNEI VLSAGSTPHIOGLTVEQAEAVVRLSCLPAFKOLIAKQVQADEQEGWLDSSSPQOTVPYILWSEETPATPIGOATHRLILLIOAFRDDR  
 Mm\_Dnchc1 3899 YDAEFQHFIRGNEI VLSAGSTPHIOGLTVEQAEAVVRLSCLPAFKOLIAKQVQADEQEGWLDSSSPQOTVPYILWSEETPATPIGOATHRLILLIOAFRDDR  
 Hs\_DNCH1 4001 LLAMAHNFVSTNLGFSFMSIMEQPLDLTHIVGTEVAPNTPVLMCSVPGYDASGHVEDLAEOQNTQITSLAIGSAGEFNQADKANTAVKSGRAWMLKNVH  
 Mm\_Dnchc1 3999 LLAMAHNFVSTNLGFSFMSIMEQPLDLTHIVGTEVAPNTPVLMCSVPGYDASGHVEDLAEOQNTQITSLAIGSAGEFNQADKANTAVKSGRAWMLKNVH  
 Hs\_DNCH1 4101 LAPGHLMOLEKLLHSLQPHACPRLEFIMEINPKVPVNLARAGSIFVFEPPPGVKANMLRFTSSIPVSRICKSPNERARLYELLAWFHAIIOERLRYAPLG  
 Mm\_Dnchc1 4099 LAPGHLMOLEKLLHSLQPHACPRLEFIMEINPKVPVNLARAGSIFVFEPPPGVKANMLRFTSSIPVSRICKSPNERARLYELLAWFHAIIOERLRYAPLG  
 Hs\_DNCH1 4201 #SKKYEFGESDLSRACDTVDWLDTPAKGRQNI SPDKIPWALSALKTMAQSIYGGVNDNEQDQLLNTFLERLFTTRSFDSSEFKLACKVDGKDIQMPDGI  
 Mm\_Dnchc1 4199 #SKKYEFGESDLSRACDTVDWLDTPAKGRQNI SPDKIPWALSALKTMAQSIYGGVNDNEQDQLLNTFLERLFTTRSFDSSEFKLACKVDGKDIQMPDGI  
 Hs\_DNCH1 4301 RREEFVQWVELLPDQTPSWLGLPNNARVLLTQGVDMISKMLKNQMLEDEDDLAYAEKERTDSTSDGRPAWRTLTHTTASNLWHLIPQTLSLHKKR  
 Mm\_Dnchc1 4299 RREEFVQWVELLPDQTPSWLGLPNNARVLLTQGVDMISKMLKNQMLEDEDDLAYAEKERTDSTSDGRPAWRTLTHTTASNLWHLIPQTLSLHKKR  
 Hs\_DNCH1 4401 TVENIKDPLFRFFEREVRKGA KLOOVRODLADVQVCEGKKTQNYLNTLINELVKGLIPRSWSHYTPAGTIVIQWVSDFSERIKQLQNI SAAASGG  
 Mm\_Dnchc1 4399 TVENIKDPLFRFFEREVRKGA KLOOVRODLADVQVCEGKKTQNYLNTLINELVKGLIPRSWSHYTPAGTIVIQWVSDFSERIKQLQNI SAAASGG

BEST AVAILABLE COPY

(Figure 9 continued)

Hs_DNCH1	4501	AKELKNIHVCLGGLFVPEAYITATROYVAQANMSLEEICLEVNVITTSQATLDACSGVGTGKLGQATCSNNKLSLSNAISTALPLTQLRWVKQTNTK
Mm_Dnchcl	4499	AKELKNIHVCLGGLFVPEAYITATROYVAQANMSLEEICLEVNVITTSQATLDACSGVGTGKLGQATCSNNKLSLSNAISTALPLTQLRWVKQTSK
Hs_DNCH1	4601	KASVVTLPVYLNFTRADLIFTVDFEATKEDPRSFYERGVAVLCDE
Mm_Dnchcl	4599	KASVVTLPVYLNFTRADLIFTVDFEATKEDPRSFYERGVAVLCDE

BEST AVAILABLE COPY

# Figure 10. Amino Acid Alignment of Human DNCH1, Mouse Dnchc1, and rat Dnchc1 Proteins –highly conserved amino acid residues.

Software used:

- Multalin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

Hs: Homo sapiens; deduced by homology  
 Mm: Mus musculus; NP\_084514  
 Rn: Rattus norvegicus; NP\_062099

Mm	1	MSPEGGG...EDGSAGLEVS	AVQNVADSVLQKHLRLKVLPLLEDGDDAPAALEAALEKSALEQMRKFLSDQVHTLVVERSTLKEDVDGDEGEKEEFTS	1
Rn	1	MSPEGGG...EDGSAGLEVS	AVQNVADSVLQKHLRLKVLPLLEDGDDAPAALEAALEKSALEQMRKFLSDQVHTLVVERSTLKEDVDGDEGEKEEFTS	1
Hs	1	MSPEGGG...EDGSAGLEVS	AVQNVADSVLQKHLRLKVLPLLEDGDDAPAALEAALEKSALEQMRKFLSDQVHTLVVERSTLKEDVDGDEGEKEEFTS	1
Consensus	1	MSPEGGG...EDGSAGLEVS	AVQNVADSVLQKHLRLKVLPLLEDGDDAPAALEAALEKSALEQMRKFLSDQVHTLVVERSTLKEDVDGDEGEKEEFTS	1
Mm	99	YNIIDIHGVKSNLSLAFIKRAPVIDADKPVSSQSLRVLTLSDDSPYETLHSTISNAVAPFFKSYIRESGKADRDGDKMAPSVEKKTAELMGLHLQQNI		
Rn	99	YNIIDIHGVKSNLSLAFIKRAPVIDADKPVSSQSLRVLTLSDDSPYETLHSTISNAVAPFFKSYIRESGKADRDGDKMAPSVEKKTAELMGLHLQQNI		
Hs	101	YNIIDIHGVKSNLSLAFIKRAPVIDADKPVSSQSLRVLTLSDDSPYETLHSTISNAVAPFFKSYIRESGKADRDGDKMAPSVEKKTAELMGLHLQQNI		
Consensus	98	YNIIDIHGVKSNLSLAFIKRAPVIDADKPVSSQSLRVLTLSDDSPYETLHSTISNAVAPFFKSYIRESGKADRDGDKMAPSVEKKTAELMGLHLQQNI		
Mm	199	EIPEISLPIHPITNVAKQCYERGEKPKVTDGDKVEDPTFINQLQSGVNRWIRIETQKVTIKDRDPASGTALQETISFWNLRLALYRIQEKRESPEVLLT		
Rn	199	EIPEISLPIHPITNVAKQCYERGEKPKVTDGDKVEDPTFINQLQSGVNRWIRIETQKVTIKDRDPASGTALQETISFWNLRLALYRIQEKRESPEVLLT		
Hs	201	EIPEISLPIHPITNVAKQCYERGEKPKVTDGDKVEDPTFINQLQSGVNRWIRIETQKVTIKDRDPASGTALQETISFWNLRLALYRIQEKRESPEVLLT		
Consensus	198	EIPEISLPIHPITNVAKQCYERGEKPKVTDGDKVEDPTFINQLQSGVNRWIRIETQKVTIKDRDPASGTALQETISFWNLRLALYRIQEKRESPEVLLT		
Mm	299	LDILKHGRRHATVVSFDTDTGLKQALETVMDYNDYNPIMKDFPPLNDLLSATELDKIRQALVAIFTHLRKIRNTKYPYIQRALRLVEAISRDLSQLLKVLTGRK		
Rn	299	LDILKHGRRHATVVSFDTDTGLKQALETVMDYNDYNPIMKDFPPLNDLLSATELDKIRQALVAIFTHLRKIRNTKYPYIQRALRLVEAISRDLSQLLKVLTGRK		
Hs	301	LDILKHGRRHATVVSFDTDTGLKQALETVMDYNDYNPIMKDFPPLNDLLSATELDKIRQALVAIFTHLRKIRNTKYPYIQRALRLVEAISRDLSQLLKVLTGRK		
Consensus	298	LDILKHGRRHATVVSFDTDTGLKQALETVMDYNDYNPIMKDFPPLNDLLSATELDKIRQALVAIFTHLRKIRNTKYPYIQRALRLVEAISRDLSQLLKVLTGRK		
Mm	399	LMHVAYEEFEKVVAVACFEVFQTDWDEYEKQLVLLRDIIVKRRRENLKVMWRINPAHRKLOARLDQMRKERRQHEOLRAVIVRVLREPQVTAQAQNGGEAP		
Rn	399	LMHVAYEEFEKVVAVACFEVFQTDWDEYEKQLVLLRDIIVKRRRENLKVMWRINPAHRKLOARLDQMRKERRQHEOLRAVIVRVLREPQVTAQAQNGGEAP		
Hs	401	LMHVAYEEFEKVVAVACFEVFQTDWDEYEKQLVLLRDIIVKRRRENLKVMWRINPAHRKLOARLDQMRKERRQHEOLRAVIVRVLREPQVTAQAQNGGEAP		
Consensus	398	LMHVAYEEFEKVVAVACFEVFQTDWDEYEKQLVLLRDIIVKRRRENLKVMWRINPAHRKLOARLDQMRKERRQHEOLRAVIVRVLREPQVTAQAQNGGEAP		
Mm	499	EPQDMKVAEVLFDAAADANITIEVNILAYENKVEVDGLDVSKEGTAEWAAMKRYDERIDRVETRTIARLDQGTAKNANEMFRIFSRFNALFVRPHIRGA		
Rn	499	EPQDMKVAEVLFDAAADANITIEVNILAYENKVEVDGLDVSKEGTAEWAAMKRYDERIDRVETRTIARLDQGTAKNANEMFRIFSRFNALFVRPHIRGA		
Hs	501	EPQDMKVAEVLFDAAADANITIEVNILAYENKVEVDGLDVSKEGTAEWAAMKRYDERIDRVETRTIARLDQGTAKNANEMFRIFSRFNALFVRPHIRGA		
Consensus	498	EPQDMKVAEVLFDAAADANITIEVNILAYENKVEVDGLDVSKEGTAEWAAMKRYDERIDRVETRTIARLDQGTAKNANEMFRIFSRFNALFVRPHIRGA		

BEST AVAILABLE COPY

(Figure 10 continued)

Mm	599	IREYOTQLIQRVKDDI	ESLHDKFKVQYPOSOQACKSHVRDLPPVSGSIIIAKQIDRLQTA	YKRRVEDVLGKGNNHVEGQKLDGDSFRUKLNTQELFD					
Rn	599	IREYOTQLIQRVKDDI	ESLHDKFKVQYPOSOQACKSHVRDLPPVSGSIIIAKQIDRLQTA	YKRRVEDVLGKGNNHVEGQKLDGDSFRUKLNTQELFD					
Hs	601	IREYOTQLIQRVKDDI	ESLHDKFKVQYPOSOQACKSHVRDLPPVSGSIIIAKQIDRLQTA	YKRRVEDVLGKGNNHVEGQKLDGDSFRUKLNTQELFD					
Consensus	598	IREYOTQLIQRVKDDI	ESLHDKFKVQYPOSOQACKSHVRDLPPVSGSIIIAKQIDRLQTA	YKRRVEDVLGKGNNHVEGQKLDGDSFRUKLNTQELFD					
Mm	699	QWARKVQQRNLGVSGRI	FTTIESARVRGRTGNVLKLVNLP	PEITLTSKVRNLKWLGRVPLAIVNKAHQANOLYPPAFSLIESVRTYERTCEKVEERN					
Rn	699	QWARKVQQRNLGVSGRI	FTTIESARVRGRTGNVLKLVNLP	PEITLTSKVRNLKWLGRVPLAIVNKAHQANOLYPPAFSLIESVRTYERTCEKVEERN					
Hs	701	QWARKVQQRNLGVSGRI	FTTIESARVRGRTGNVLKLVNLP	PEITLTSKVRNLKWLGRVPLAIVNKAHQANOLYPPAFSLIESVRTYERTCEKVEERN					
Consensus	698	QWARKVQQRNLGVSGRI	FTTIESARVRGRTGNVLKLVNLP	PEITLTSKVRNLKWLGRVPLAIVNKAHQANOLYPPAFSLIESVRTYERTCEKVEERN					
Mm	799	ISLAVAGLKEVQALL	AEQIALWESYKLDPPYVQRLAETVFNQKQVDDLLIEEKIDLEVS	LETCHNDHKTFSILLNRVQKAVDDLNLSYSLPIW					
Rn	799	ISLAVAGLKEVQALL	AEQIALWESYKLDPPYVQRLAETVFNQKQVDDLLIEEKIDLEVS	LETCHNDHKTFSILLNRVQKAVDDLNLSYSLPIW					
Hs	801	ISLAVAGLKEVQALL	AEQIALWESYKLDPPYVQRLAETVFNQKQVDDLLIEEKIDLEVS	LETCHNDHKTFSILLNRVQKAVDDLNLSYSLPIW					
Consensus	798	ISLAVAGLKEVQALL	AEQIALWESYKLDPPYVQRLAETVFNQKQVDDLLIEEKIDLEVS	LETCHNDHKTFSILLNRVQKAVDDLNLSYSLPIW					
Mm	899	NKLDHEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHEL	RIITNOVLYLNPPIEECRKLYQOEMFAMKVVLSLPRIO					
Rn	899	NKLDHEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHEL	RIITNOVLYLNPPIEECRKLYQOEMFAMKVVLSLPRIO					
Hs	901	NKLDHEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHEL	RIITNOVLYLNPPIEECRKLYQOEMFAMKVVLSLPRIO					
Consensus	898	NKLDHEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHEL	RIITNOVLYLNPPIEECRKLYQOEMFAMKVVLSLPRIO					
Mm	999	SQRYQGVHYELTEEEKFYRNAL	TRMPDGPVAALESYS	SAVNGIVTEVEQYKVMVLYQYQCLMDQAEINIYRLGEDLNKQVALLVQIRKARGTDFDNETKK					
Rn	999	SQRYQGVHYELTEEEKFYRNAL	TRMPDGPVAALESYS	SAVNGIVTEVEQYKVMVLYQYQCLMDQAEINIYRLGEDLNKQVALLVQIRKARGTDFDNETKK					
Hs	1001	SQRYQGVHYELTEEEKFYRNAL	TRMPDGPVAALESYS	SAVNGIVTEVEQYKVMVLYQYQCLMDQAEINIYRLGEDLNKQVALLVQIRKARGTDFDNETKK					
Consensus	997	SQRYQGVHYELTEEEKFYRNAL	TRMPDGPVAALESYS	SAVNGIVTEVEQYKVMVLYQYQCLMDQAEINIYRLGEDLNKQVALLVQIRKARGTDFDNETKK					
Mm	1099	EFGPWVIDYGVQSVKVNLYK	SDWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVD	TASTSDAVTITTVVQSLKRIKQFEKQVLEYRNGQRLLEKO					
Rn	1099	EFGPWVIDYGVQSVKVNLYK	SDWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVD	TASTSDAVTITTVVQSLKRIKQFEKQVLEYRNGQRLLEKO					
Hs	1101	EFGPWVIDYGVQSVKVNLYK	SDWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVD	TASTSDAVTITTVVQSLKRIKQFEKQVLEYRNGQRLLEKO					
Consensus	1097	EFGPWVIDYGVQSVKVNLYK	SDWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVD	TASTSDAVTITTVVQSLKRIKQFEKQVLEYRNGQRLLEKO					
Mm	1199	RFQPPPSWLYIDNTEG	WGAFNDRKRD	SAIQOOVANLQMKI	VOEDRAVESRTTDLTDWEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA				
Rn	1199	RFQPPPSWLYIDNTEG	WGAFNDRKRD	SAIQOOVANLQMKI	VOEDRAVESRTTDLTDWEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA				
Hs	1201	RFQPPPSWLYIDNTEG	WGAFNDRKRD	SAIQOOVANLQMKI	VOEDRAVESRTTDLTDWEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA				
Consensus	1197	RFQPPPSWLYIDNTEG	WGAFNDRKRD	SAIQOOVANLQMKI	VOEDRAVESRTTDLTDWEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA				
Mm	1299	KEALELDTGGLSGSEER	VQVALLQKGVWSEL	SKWEGIQDKKQPPWVSQVPRKLRQNLGLLQNLK	NFPARLQVASYEFVQRLKGVYKNTNMLV				
Rn	1299	KEALELDTGGLSGSEER	VQVALLQKGVWSEL	SKWEGIQDKKQPPWVSQVPRKLRQNLGLLQNLK	NFPARLQVASYEFVQRLKGVYKNTNMLV				
Hs	1301	KEALELDTGGLSGSEER	VQVALLQKGVWSEL	SKWEGIQDKKQPPWVSQVPRKLRQNLGLLQNLK	NFPARLQVASYEFVQRLKGVYKNTNMLV				
Consensus	1297	KEALELDTGGLSGSEER	VQVALLQKGVWSEL	SKWEGIQDKKQPPWVSQVPRKLRQNLGLLQNLK	NFPARLQVASYEFVQRLKGVYKNTNMLV				
Mm	1399	TELKSEALKDRHWKQ	MLKRLHVN	NWVSELTTLGQIDVDVLDQKNEA	LVKQVLAQCEMAL	EEELKQIREVNTYELDLNVYQNKCR	LIRGWDDDLFNKVKKEH		
Rn	1399	TELKSEALKDRHWKQ	MLKRLHVN	NWVSELTTLGQIDVDVLDQKNEA	LVKQVLAQCEMAL	EEELKQIREVNTYELDLNVYQNKCR	LIRGWDDDLFNKVKKEH		
Hs	1401	TELKSEALKDRHWKQ	MLKRLHVN	NWVSELTTLGQIDVDVLDQKNEA	LVKQVLAQCEMAL	EEELKQIREVNTYELDLNVYQNKCR	LIRGWDDDLFNKVKKEH		
Consensus	1397	TELKSEALKDRHWKQ	MLKRLHVN	NWVSELTTLGQIDVDVLDQKNEA	LVKQVLAQCEMAL	EEELKQIREVNTYELDLNVYQNKCR	LIRGWDDDLFNKVKKEH		
Mm	1499	INVSAMKLSPYK	VFEEDALS	WEDKLNRI	NALFDVWIDVORRWY	LEGITFGSDIKHLL	VEVQRFOSISTEFALMKKVS	KLPLVMDVNL	IQGVORS
Rn	1499	INVSAMKLSPYK	VFEEDALS	WEDKLNRI	NALFDVWIDVORRWY	LEGITFGSDIKHLL	VEVQRFOSISTEFALMKKVS	KLPLVMDVNL	IQGVORS
Hs	1501	INVSAMKLSPYK	VFEEDALS	WEDKLNRI	NALFDVWIDVORRWY	LEGITFGSDIKHLL	VEVQRFOSISTEFALMKKVS	KLPLVMDVNL	IQGVORS
Consensus	1496	INVSAMKLSPYK	VFEEDALS	WEDKLNRI	NALFDVWIDVORRWY	LEGITFGSDIKHLL	VEVQRFOSISTEFALMKKVS	KLPLVMDVNL	IQGVORS

BEST AVAILABLE COPY



(Figure 10 continued)

Mm	1599	LERLADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLOHFKKMFAGVSSIIINEDSNVLGITSSREGGEVMEKTPVSI TEHPKINE
Rn	1599	LERLADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLOHFKKMFAGVSSIIINEDSNVLGITSSREGGEVMEKTPVSI TEHPKINE
Hs	1601	LERLADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLOHFKKMFAGVSSIIINEDSNVLGITSSREGGEVMEKTPVSI TEHPKINE
Consensus	1596	LERLADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLOHFKKMFAGVSSIIINEDSNVLGITSSREGGEVMEKTPVSI TEHPKINE
Mm	1699	GLTLVEKEMRVTLAKLLAESVTEVEIFGKATSIDPNTYITWDKVOAQOVLVLSAQIAMSBNVENALSNVGGGDDVGPLOSIVLSNVEVTNLVLADSVLMQC
Rn	1699	GLTLVEKEMRVTLAKLLAESVTEVEIFGKATSIDPNTYITWDKVOAQOVLVLSAQIAMSBNVENALSNVGGGDDVGPLOSIVLSNVEVTNLVLADSVLMQC
Hs	1701	GLTLVEKEMRVTLAKLLAESVTEVEIFGKATSIDPNTYITWDKVOAQOVLVLSAQIAMSBNVENALSNVGGGDDVGPLOSIVLSNVEVTNLVLADSVLMQC
Consensus	1696	GLTLVEKEMRVTLAKLLAESVTEVEIFGKATSIDPNTYITWDKVOAQOVLVLSAQIAMSBNVENALSNVGGGDDVGPLOSIVLSNVEVTNLVLADSVLMQC
Mm	1799	PLPRLRRKLEHLITELVHORVTRSLIKSKIDNAKSEWILSQMRFXFDPKOTDVLQQLSIQMANAKNMGFEYXIGVQDKLVQVTELTORCYLTMTQALEARL
Rn	1799	PLPRLRRKLEHLITELVHORVTRSLIKSKIDNAKSEWILSQMRFXFDPKOTDVLQQLSIQMANAKNMGFEYXIGVQDKLVQVTELTORCYLTMTQALEARL
Hs	1801	PLPRLRRKLEHLITELVHORVTRSLIKSKIDNAKSEWILSQMRFXFDPKOTDVLQQLSIQMANAKNMGFEYXIGVQDKLVQVTELTORCYLTMTQALEARL
Consensus	1796	PLPRLRRKLEHLITELVHORVTRSLIKSKIDNAKSEWILSQMRFXFDPKOTDVLQQLSIQMANAKNMGFEYXIGVQDKLVQVTELTORCYLTMTQALEARL
Mm	1899	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVQCIQALREHSNPNVDKTSAPITCE
Rn	1899	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVQCIQALREHSNPNVDKTSAPITCE
Hs	1901	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVQCIQALREHSNPNVDKTSAPITCE
Consensus	1896	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVQCIQALREHSNPNVDKTSAPITCE
Mm	1999	LINKQVKVSPDMAIFITWMPGYAGRSNLPDNLKLLFRSLAMTKPDRQLIAQVWLXQGPRTAEVLANKIVPPFKLCDEQLSSQSHYDFGIRALKSVLVA
Rn	1999	LINKQVKVSPDMAIFITWMPGYAGRSNLPDNLKLLFRSLAMTKPDRQLIAQVWLXQGPRTAEVLANKIVPPFKLCDEQLSSQSHYDFGIRALKSVLVA
Hs	2001	LINKQVKVSPDMAIFITWMPGYAGRSNLPDNLKLLFRSLAMTKPDRQLIAQVWLXQGPRTAEVLANKIVPPFKLCDEQLSSQSHYDFGIRALKSVLVA
Consensus	1996	LINKQVKVSPDMAIFITWMPGYAGRSNLPDNLKLLFRSLAMTKPDRQLIAQVWLXQGPRTAEVLANKIVPPFKLCDEQLSSQSHYDFGIRALKSVLVA
Mm	2099	SNVKKRERLOKIKREKEERGEAVDEGEIAENLPEQELLQSVCEWVPPKIVAEDIPIILFSLSDVPFGVQYHRCGEMTALREELKKVQCEMYLTYGDEGEVNG
Rn	2099	SNVKKRERLOKIKREKEERGEAVDEGEIAENLPEQELLQSVCEWVPPKIVAEDIPIILFSLSDVPFGVQYHRCGEMTALREELKKVQCEMYLTYGDEGEVNG
Hs	2101	SNVKKRERLOKIKREKEERGEAVDEGEIAENLPEQELLQSVCEWVPPKIVAEDIPIILFSLSDVPFGVQYHRCGEMTALREELKKVQCEMYLTYGDEGEVNG
Consensus	2096	SNVKKRERLOKIKREKEERGEAVDEGEIAENLPEQELLQSVCEWVPPKIVAEDIPIILFSLSDVPFGVQYHRCGEMTALREELKKVQCEMYLTYGDEGEVNG
Mm	2199	GNWVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKAISKDHLYCTLDPNTREMTDGLFTHVLKRIIDNVRGELQKRW
Rn	2199	GNWVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKAISKDHLYCTLDPNTREMTDGLFTHVLKRIIDNVRGELQKRW
Hs	2201	GNWVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKAISKDHLYCTLDPNTREMTDGLFTHVLKRIIDNVRGELQKRW
Consensus	2196	GNWVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKAISKDHLYCTLDPNTREMTDGLFTHVLKRIIDNVRGELQKRW
Mm	2299	LVFDGVDPEWVENLNSVLDNKKLLTPNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDDEGEDEAQRKRG
Rn	2299	LVFDGVDPEWVENLNSVLDNKKLLTPNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDDEGEDEAQRKRG
Hs	2301	LVFDGVDPEWVENLNSVLDNKKLLTPNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDDEGEDEAQRKRG
Consensus	2296	LVFDGVDPEWVENLNSVLDNKKLLTPNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDDEGEDEAQRKRG
Mm	2399	KEDGEEAASPMLOIQORDATTIMQPYFTSYNGLVTKALEHAFKLEHIMDLTRLCIGSLFSMHQACRVAAQVNAHPDPFPMQIEQIERVYQIRVLVVAIIW
Rn	2399	KEDGEEAASPMLOIQORDATTIMQPYFTSYNGLVTKALEHAFKLEHIMDLTRLCIGSLFSMHQACRVAAQVNAHPDPFPMQIEQIERVYQIRVLVVAIIW
Hs	2401	KEDGEEAASPMLOIQORDATTIMQPYFTSYNGLVTKALEHAFKLEHIMDLTRLCIGSLFSMHQACRVAAQVNAHPDPFPMQIEQIERVYQIRVLVVAIIW
Consensus	2396	KEDGEEAASPMLOIQORDATTIMQPYFTSYNGLVTKALEHAFKLEHIMDLTRLCIGSLFSMHQACRVAAQVNAHPDPFPMQIEQIERVYQIRVLVVAIIW
Mm	2499	SLSGDSRLKMRALGEYIRRTITVPLTPAPNPIIDYEVSISGEWSPQAKVPOIEVEVTHKVAAPDVVVPTDPTVRHEALLYTLAEHKLPLVLCGPGGSG
Rn	2499	SLSGDSRLKMRALGEYIRRTITVPLTPAPNPIIDYEVSISGEWSPQAKVPOIEVEVTHKVAAPDVVVPTDPTVRHEALLYTLAEHKLPLVLCGPGGSG
Hs	2501	SLSGDSRLKMRALGEYIRRTITVPLTPAPNPIIDYEVSISGEWSPQAKVPOIEVEVTHKVAAPDVVVPTDPTVRHEALLYTLAEHKLPLVLCGPGGSG
Consensus	2496	SLSGDSRLKMRALGEYIRRTITVPLTPAPNPIIDYEVSISGEWSPQAKVPOIEVEVTHKVAAPDVVVPTDPTVRHEALLYTLAEHKLPLVLCGPGGSG

BEST AVAILABLE COPY



(Figure 10 continued)

Mm	2599	KTMTLFSALRALPDMEVGLNFSSATTPELLKKTEDHYCEYRRTPNGVVLAVOLGKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFWRTSDQW
Rn	2599	KTMTLFSALRALPDMEVGLNFSSATTPELLKKTEDHYCEYRRTPNGVVLAVOLGKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFWRTSDQW
Hs	2601	KTMTLFSALRALPDMEVGLNFSSATTPELLKKTEDHYCEYRRTPNGVVLAVOLGKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFWRTSDQW
Consensus	2595	KTMTLFSALRALPDMEVGLNFSSATTPELLKKTEDHYCEYRRTPNGVVLAVOLGKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFWRTSDQW
Mm	2699	VKLERIQEVGACNPPTDGRPLSHRFLRHVPVYVVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTMSQERFTQDTPHVIYSPREMT
Rn	2699	VKLERIQEVGACNPPTDGRPLSHRFLRHVPVYVVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTMSQERFTQDTPHVIYSPREMT
Hs	2701	VKLERIQEVGACNPPTDGRPLSHRFLRHVPVYVVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTMSQERFTQDTPHVIYSPREMT
Consensus	2695	VKLERIQEVGACNPPTDGRPLSHRFLRHVPVYVVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTMSQERFTQDTPHVIYSPREMT
Mm	2799	RWVGIFEARPLETLPVEGLIRIWAHEALFLFODRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Rn	2799	RWVGIFEARPLETLPVEGLIRIWAHEALFLFODRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Hs	2801	RWVGIFEARPLETLPVEGLIRIWAHEALFLFODRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Consensus	2795	RWVGIFEARPLETLPVEGLIRIWAHEALFLFODRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Mm	2899	YEEELDVPLVLFNEVLHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGDEDFEDLRTVLRSSGCKNEKIAFIMDES NVL
Rn	2899	YEEELDVPLVLFNEVLHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGDEDFEDLRTVLRSSGCKNEKIAFIMDES NVL
Hs	2901	YEEELDVPLVLFNEVLHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGDEDFEDLRTVLRSSGCKNEKIAFIMDES NVL
Consensus	2895	YEEELDVPLVLFNEVLHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGDEDFEDLRTVLRSSGCKNEKIAFIMDES NVL
Mm	2999	DSGFLENNMTLLANGEVPGLFEGDEVATLNTQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKORAAATSPALFNRCVLNWFCDWSTE
Rn	2999	DSGFLENNMTLLANGEVPGLFEGDEVATLNTQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKORAAATSPALFNRCVLNWFCDWSTE
Hs	3001	DSGFLENNMTLLANGEVPGLFEGDEVATLNTQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKORAAATSPALFNRCVLNWFCDWSTE
Consensus	2995	DSGFLENNMTLLANGEVPGLFEGDEVATLNTQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKORAAATSPALFNRCVLNWFCDWSTE
Mm	3099	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIIVNSCVFVHQTLOHANAALAKRGGRMTATTPRHYLDFINHYANLFEHKESELEEQQMH
Rn	3099	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIIVNSCVFVHQTLOHANAALAKRGGRMTATTPRHYLDFINHYANLFEHKESELEEQQMH
Hs	3101	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIIVNSCVFVHQTLOHANAALAKRGGRMTATTPRHYLDFINHYANLFEHKESELEEQQMH
Consensus	3095	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIIVNSCVFVHQTLOHANAALAKRGGRMTATTPRHYLDFINHYANLFEHKESELEEQQMH
Mm	3199	LAVGLRKIKETVDQVEELRDRLRIKSOQLELVKNAANDKLLKMKVQDQOEAKKKVWSQETQEOQLHKQEVIAADQMSWKEDLDKVEPAVIEAQNAAVKSIR
Rn	3199	LAVGLRKIKETVDQVEELRDRLRIKSOQLELVKNAANDKLLKMKVQDQOEAKKKVWSQETQEOQLHKQEVIAADQMSWKEDLDKVEPAVIEAQNAAVKSIR
Hs	3201	LAVGLRKIKETVDQVEELRDRLRIKSOQLELVKNAANDKLLKMKVQDQOEAKKKVWSQETQEOQLHKQEVIAADQMSWKEDLDKVEPAVIEAQNAAVKSIR
Consensus	3195	LAVGLRKIKETVDQVEELRDRLRIKSOQLELVKNAANDKLLKMKVQDQOEAKKKVWSQETQEOQLHKQEVIAADQMSWKEDLDKVEPAVIEAQNAAVKSIR
Mm	3299	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIINRENFIPITVNFSAEETSDAIKREKKNKYNMSPSYNYEIVNRASLACGPMVKWATAQL
Rn	3299	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIINRENFIPITVNFSAEETSDAIKREKKNKYNMSPSYNYEIVNRASLACGPMVKWATAQL
Hs	3301	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIINRENFIPITVNFSAEETSDAIKREKKNKYNMSPSYNYEIVNRASLACGPMVKWATAQL
Consensus	3295	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIINRENFIPITVNFSAEETSDAIKREKKNKYNMSPSYNYEIVNRASLACGPMVKWATAQL
Mm	3399	NYADMILKRVPELRLNELQKLEDDAKNDQKQANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAAVEAKVNRSTALLKSLSAERERWEKTSFTFKNQ
Rn	3399	NYADMILKRVPELRLNELQKLEDDAKNDQKQANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAAVEAKVNRSTALLKSLSAERERWEKTSFTFKNQ
Hs	3401	NYADMILKRVPELRLNELQKLEDDAKNDQKQANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAAVEAKVNRSTALLKSLSAERERWEKTSFTFKNQ
Consensus	3395	NYADMILKRVPELRLNELQKLEDDAKNDQKQANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAAVEAKVNRSTALLKSLSAERERWEKTSFTFKNQ
Mm	3499	STIAGCCLLSAAFIAYAGYEDQOMRONLFTTWSHHLQQANIQERTDIARTEYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI
Rn	3499	STIAGCCLLSAAFIAYAGYEDQOMRONLFTTWSHHLQQANIQERTDIARTEYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI
Hs	3501	STIAGCCLLSAAFIAYAGYEDQOMRONLFTTWSHHLQQANIQERTDIARTEYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI
Consensus	3495	STIAGCCLLSAAFIAYAGYEDQOMRONLFTTWSHHLQQANIQERTDIARTEYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI

UNRELIABLE COPY

10/527769

(Figure 10 continued)

Mm	3599	YNEYKDKRIKTRTSFLDDAERKNLESALRFGNPLIVQDVESYDPVLPVLAENREVRTGRVLTITLGDODIDLSPSFVFLSTROPTVEFPDLCRSRVTEVN
Rn	3599	YNEYKDKRIKTRTSFLDDAERKNLESALRFGNPLIVQDVESYDPVLPVLAENREVRTGRVLTITLGDODIDLSPSFVFLSTROPTVEFPDLCRSRVTEVN
Hs	3601	YNEYKDKRIKTRTSFLDDAERKNLESALRFGNPLIVQDVESYDPVLPVLAENREVRTGRVLTITLGDODIDLSPSFVFLSTROPTVEFPDLCRSRVTEVN
Consensus	3595	YNEYKDKRIKTRTSFLDDAERKNLESALRFGNPLIVQDVESYDPVLPVLAENREVRTGRVLTITLGDODIDLSPSFVFLSTROPTVEFPDLCRSRVTEVN
Mm	3699	FTWTRSLQSCCLNEVLKAERPDVDEKRSLLKALQGEFQRLRLQLEKSLQAALNEVGRILDDTTITLLEMLKREAAEVTRKVEETDIVMOEVTVSQQ
Rn	3699	FTWTRSLQSCCLNEVLKAERPDVDEKRSLLKALQGEFQRLRLQLEKSLQAALNEVGRILDDTTITLLEMLKREAAEVTRKVEETDIVMOEVTVSQQ
Hs	3701	FTWTRSLQSCCLNEVLKAERPDVDEKRSLLKALQGEFQRLRLQLEKSLQAALNEVGRILDDTTITLLEMLKREAAEVTRKVEETDIVMOEVTVSQQ
Consensus	3695	FTWTRSLQSCCLNEVLKAERPDVDEKRSLLKALQGEFQRLRLQLEKSLQAALNEVGRILDDTTITLLEMLKREAAEVTRKVEETDIVMOEVTVSQQ
Mm	3799	YLPSTACSSIIYFTMESLKQVHFTYQVSLQFFLDIYHNVLNENPNLRKAGTDHTQRLSVITKDLFQVAFNRVARGMHQDHTITFAMLLARIKLKGTGVEPT
Rn	3799	YLPSTACSSIIYFTMESLKQVHFTYQVSLQFFLDIYHNVLNENPNLRKAGTDHTQRLSVITKDLFQVAFNRVARGMHQDHTITFAMLLARIKLKGTGVEPT
Hs	3801	YLPSTACSSIIYFTMESLKQVHFTYQVSLQFFLDIYHNVLNENPNLRKAGTDHTQRLSVITKDLFQVAFNRVARGMHQDHTITFAMLLARIKLKGTGVEPT
Consensus	3795	YLPSTACSSIIYFTMESLKQVHFTYQVSLQFFLDIYHNVLNENPNLRKAGTDHTQRLSVITKDLFQVAFNRVARGMHQDHTITFAMLLARIKLKGTGVEPT
Mm	3899	YDAEFQHFHFKGKEIVLSAGSTPKIQLGTVQEAQAVRLSLCPAFKDIKAVQADEQFGIMLSSSSPEQTPVYPLWSEETPTPIGQATHRLLLIOAFRDR
Rn	3899	YDAEFQHFHFKGKEIVLSAGSTPKIQLGTVQEAQAVRLSLCPAFKDIKAVQADEQFGIMLSSSSPEQTPVYPLWSEETPTPIGQATHRLLLIOAFRDR
Hs	3901	YDAEFQHFHFKGKEIVLSAGSTPKIQLGTVQEAQAVRLSLCPAFKDIKAVQADEQFGIMLSSSSPEQTPVYPLWSEETPTPIGQATHRLLLIOAFRDR
Consensus	3893	YDAEFQHFHFKGKEIVLSAGSTPKIQLGTVQEAQAVRLSLCPAFKDIKAVQADEQFGIMLSSSSPEQTPVYPLWSEETPTPIGQATHRLLLIOAFRDR
Mm	3999	FLANAHMFVSTNLGESFMSINEQPLDITHTLVGTEVKNPNTVLMCSVPGYDASGHVEDLAEEQNTQITSLAIGSAEGFNQADKAINTAVKSGRWVLKNVH
Rn	3999	FLANAHMFVSTNLGESFMSINEQPLDITHTLVGTEVKNPNTVLMCSVPGYDASGHVEDLAEEQNTQITSLAIGSAEGFNQADKAINTAVKSGRWVLKNVH
Hs	4001	FLANAHMFVSTNLGESFMSINEQPLDITHTLVGTEVKNPNTVLMCSVPGYDASGHVEDLAEEQNTQITSLAIGSAEGFNQADKAINTAVKSGRWVLKNVH
Consensus	3991	FLANAHMFVSTNLGESFMSINEQPLDITHTLVGTEVKNPNTVLMCSVPGYDASGHVEDLAEEQNTQITSLAIGSAEGFNQADKAINTAVKSGRWVLKNVH
Mm	4099	LAPGMWLMQLEKKLHSLQPHACFRLFTIMEINPKVPVALLRAGRI FVEPPPGVKANMLRTFSSI PVSRIKCSNPERARLYVLLAWFHAI IQERLRYAPLG
Rn	4099	LAPGMWLMQLEKKLHSLQPHACFRLFTIMEINPKVPVALLRAGRI FVEPPPGVKANMLRTFSSI PVSRIKCSNPERARLYVLLAWFHAI IQERLRYAPLG
Hs	4101	LAPGMWLMQLEKKLHSLQPHACFRLFTIMEINPKVPVALLRAGRI FVEPPPGVKANMLRTFSSI PVSRIKCSNPERARLYVLLAWFHAI IQERLRYAPLG
Consensus	4091	LAPGMWLMQLEKKLHSLQPHACFRLFTIMEINPKVPVALLRAGRI FVEPPPGVKANMLRTFSSI PVSRIKCSNPERARLYVLLAWFHAI IQERLRYAPLG
Mm	4199	MSKKYFEGESDLRSACDVTVDLDDTAKGRQNI SPDKI PWSAUKTILMAQSI YGGRVDNEFDQRLNLTFLERLFTTRESFDESEFKLACKVDGHKDIQMPDGI
Rn	4199	MSKKYFEGESDLRSACDVTVDLDDTAKGRQNI SPDKI PWSAUKTILMAQSI YGGRVDNEFDQRLNLTFLERLFTTRESFDESEFKLACKVDGHKDIQMPDGI
Hs	4201	MSKKYFEGESDLRSACDVTVDLDDTAKGRQNI SPDKI PWSAUKTILMAQSI YGGRVDNEFDQRLNLTFLERLFTTRESFDESEFKLACKVDGHKDIQMPDGI
Consensus	4190	MSKKYFEGESDLRSACDVTVDLDDTAKGRQNI SPDKI PWSAUKTILMAQSI YGGRVDNEFDQRLNLTFLERLFTTRESFDESEFKLACKVDGHKDIQMPDGI
Mm	4299	RREEFVQWVELLPDAQTPSHLGLPNNAERVLITTCQVDNI SKMLKKQMLEDEDDLAAYAEKTEKTRDSTDGPRAMWRTLHTTASNWLHLI PQTLSPLKR
Rn	4299	RREEFVQWVELLPDAQTPSHLGLPNNAERVLITTCQVDNI SKMLKKQMLEDEDDLAAYAEKTEKTRDSTDGPRAMWRTLHTTASNWLHLI PQTLSPLKR
Hs	4301	RREEFVQWVELLPDAQTPSHLGLPNNAERVLITTCQVDNI SKMLKKQMLEDEDDLAAYAEKTEKTRDSTDGPRAMWRTLHTTASNWLHLI PQTLSPLKR
Consensus	4290	RREEFVQWVELLPDAQTPSHLGLPNNAERVLITTCQVDNI SKMLKKQMLEDEDDLAAYAEKTEKTRDSTDGPRAMWRTLHTTASNWLHLI PQTLSPLKR
Mm	4399	TVENIKDPLFRFFEREVKNKAKLLQDVRODLADVQVCEGKKKQTYLRTLINELVKGLIPRSWSHYTVAGWTVIQWVSDFSERIKOLONISQAAASGG
Rn	4399	TVENIKDPLFRFFEREVKNKAKLLQDVRODLADVQVCEGKKKQTYLRTLINELVKGLIPRSWSHYTVAGWTVIQWVSDFSERIKOLONISQAAASGG
Hs	4401	TVENIKDPLFRFFEREVKNKAKLLQDVRODLADVQVCEGKKKQTYLRTLINELVKGLIPRSWSHYTVAGWTVIQWVSDFSERIKOLONISQAAASGG
Consensus	4390	TVENIKDPLFRFFEREVKNKAKLLQDVRODLADVQVCEGKKKQTYLRTLINELVKGLIPRSWSHYTVAGWTVIQWVSDFSERIKOLONISQAAASGG

NOT AVAILABLE COPY

10/527769

(Figure 10 continued)

Mm	4499	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Rn	4499	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Hs	4501	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Consensus	4490	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Mm	4599	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVICTE
Rn	4599	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVICTE
Hs	4601	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVICTE
Consensus	4590	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVICTE

Percentage of identical amino acid residues: 95%

Percentage of identical and similar amino acid residues: 96%

BEST AVAILABLE COPY

## Figure 11. Amino Acid Alignment of Mouse, and Human Dynein Intermediate Chain 1 Proteins –Highly Conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

NP_034193.1 (mouse)	1	MSDKSDLKAELEKRLQRLAQIREKKRKEERKKKEADMQQKKEPVQDDSDLDKRKRETE
NP_004402.1 (human)	1	MSDKSDLKAELEKRLQRLAQIREKKRKEERKKKEADMQQKKEPVQDDSDLDKRKRETE
Consensus	1	MSDKSDLKAELEKRLQRLAQIREKKRKEERKKKEADMQQKKEPVQDDSDLDKRKRETE
NP_034193.1 (mouse)	61	ALLQSIGISPEPLV.....PTPMSFSSKSVSTPSHAGSQDSGDLGPI
NP_004402.1 (human)	61	ALLQSIGISPEPLVQPLHFLTWDTCYFHYLVPTPMSFSSKSVSTPSHAGSQDSGDLGPI
Consensus	61	ALLQSIGISPEPLV.....PTPMSFSSKSVSTPSHAGSQDSGDLGPI
NP_034193.1 (mouse)	104	TRTLQWDTPSVLQLQSDSELGRLHLKLGVSQVTVQDFLPREVVSYSKETQTPLATHQSE
NP_004402.1 (human)	121	TRTLQWDTPSVLQLQSDSELGRLHLKLGVSQVTVQDFLPREVVSYSKETQTPLATHQSE
Consensus	103	TRTLQWDTPSVLQLQSDSELGRLHLKLGVSQVTVQDFLPREVVSYSKETQTPLATHQSE
NP_034193.1 (mouse)	164	EDEEDEEMVEPKHGHQDSELENCHKKQETKEAPPRELTEEEKQQLHSEEFLLFFDRTIRV
NP_004402.1 (human)	181	EDEEDEEMVESKGGQDSELENCHKKQETKEAPPRELTEEEKQQLHSEEFLLFFDRTIRV
Consensus	163	EDEEDEEMVEPKHGHQDSELENCHKKQETKEAPPRELTEEEKQQLHSEEFLLFFDRTIRV
NP_034193.1 (mouse)	224	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRQFYDEHWSKHRVVTCDMSLQYF
NP_004402.1 (human)	241	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRQFYDEHWSKHRVVTCDMSLQYF
Consensus	221	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRQFYDEHWSKHRVVTCDMSLQYF
NP_034193.1 (mouse)	284	ELMVASYSNNEDAPHEPDGVALVWNNMKFKKTTPYVVFHCQSSVMSVCFARFHPNLVVGGT
NP_004402.1 (human)	301	ELMVASYSNNEDAPHEPDGVALVWNNMKFKKTTPYVVFHCQSSVMSVCFARFHPNLVVGGT
Consensus	281	ELMVASYSNNEDAPHEPDGVALVWNNMKFKKTTPYVVFHCQSSVMSVCFARFHPNLVVGGT
NP_034193.1 (mouse)	344	YSGQIVLWDRSHRRTPVQRTPLSAAATHPVYCVHVVGTHHARNLITVSTDGKMCWSL
NP_004402.1 (human)	361	YSGQIVLWDRSHRRTPVQRTPLSAAATHPVYCVHVVGTHHARNLITVSTDGKMCWSL
Consensus	341	YSGQIVLWDRSHRRTPVQRTPLSAAATHPVYCVHVVGTHHARNLITVSTDGKMCWSL
NP_034193.1 (mouse)	404	DMLSTPQESMELVYNKSKPVAVTGMAFPTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_004402.1 (human)	421	DMLSTPQESMELVYNKSKPVAVTGMAFPTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
Consensus	401	DMLSTPQESMELVYNKSKPVAVTGMAFPTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_034193.1 (mouse)	464	EGHQGPVTGINCHMAVGPIDFSHLFTSSFDWTVKLWTTKHNKPLYSEDNADYVYDVMW
NP_004402.1 (human)	481	EGHQGPVTGINCHMAVGPIDFSHLFTSSFDWTVKLWTTKHNKPLYSEDNADYVYDVMW
Consensus	461	EGHQGPVTGINCHMAVGPIDFSHLFTSSFDWTVKLWTTKHNKPLYSEDNADYVYDVMW
NP_034193.1 (mouse)	524	SPVHPALFACVDGMGRDLWNLNNDTEVPTASVAIEGASALNRVRWAQAGKEVAVGDSEG
NP_004402.1 (human)	541	SPVHPALFACVDGMGRDLWNLNNDTEVPTASVAIEGASALNRVRWAQAGKEVAVGDSEG
Consensus	521	SPVHPALFACVDGMGRDLWNLNNDTEVPTASVAIEGASALNRVRWAQAGKEVAVGDSEG
NP_034193.1 (mouse)	584	RIWNYDVGELAVPHNDEWTRFARTLVEIRANRADSEEGAVELAA
NP_004402.1 (human)	601	RIWNYDVGELAVPHNDEWTRFARTLVEIRANRADSEEGAVELAA
Consensus	581	RIWNYDVGELAVPHNDEWTRFARTLVEIRANRADSEEGAVELAA

Amino acid identity: 88%

Amino acid similarity: 89%

UNRELEASABLE COPY

## Figure 12. Amino Acid Alignment of Mouse, Rattus Norvegicus, and Human Dynein Intermediate Chain1 Proteins –Highly Conserved Amino Acid Residues.

Software used:

MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

		<b>1M</b>
NP_034193.1(mouse)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEEERKKKEADMQQKKEPVQDDSLDRKRRETE
NP_004402.1(human)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEEERKKKEADMQQKKEPVQDDSLDRKRRETE
NP_062107.1(rat)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEEERKKKEADMQQKKEPVQDDSLDRKRRETE
Consensus	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEEERKKKEADMQQKKEPVQDDSLDRKRRETE
NP_034193.1(mouse)	61	ALLQSIGISPEPPLV.....PTMSPSSKSVSTFSLAGSQDSDGLGPI
NP_004402.1(human)	61	ALLQSIGISPEPPLVQPLHFLTWDTCTCYFHYLVPTMSPSSKSVSTFSEAGSQDSDGLGPI
NP_062107.1(rat)	61	ALLQSIGISPEPPLVQPLHFLTWDTCTCYFHYLVPTMSPSSKSVSTFSEAGSQDSDGLGPI
Consensus	61	ALLQSIGISPEPPLVQPLHFLTWDTCTCYFHYLVPTMSPSSKSVSTFSLAGSQDSDGLGPI
		<b>140E 157F 164B 174A</b>
NP_034193.1(mouse)	104	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
NP_004402.1(human)	121	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
NP_062107.1(rat)	121	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
Consensus	120	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
NP_034193.1(mouse)	164	EDEEDEEMVEPKGHDSLELNCCKKQETKEAPPRELTEEEKQQILHSEEFLLFFDRTIRV
NP_004402.1(human)	181	EDEEDEEMVEPKGHDSLELNCCKKQETKEAPPRELTEEEKQQILHSEEFLLFFDRTIRV
NP_062107.1(rat)	179	EDEEDEEMVEPKGHDSLELNCCKKQETKEAPPRELTEEEKQQILHSEEFLLFFDRTIRV
Consensus	180	EDEEDEEMVEPKGHDSLELNCCKKQETKEAPPRELTEEEKQQILHSEEFLLFFDRTIRV
		<b>260L</b>
NP_034193.1(mouse)	224	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
NP_004402.1(human)	241	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
NP_062107.1(rat)	239	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
Consensus	238	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
		<b>331T</b>
NP_034193.1(mouse)	284	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGTT
NP_004402.1(human)	301	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGTT
NP_062107.1(rat)	299	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGTT
Consensus	298	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGTT
NP_034193.1(mouse)	344	YSGQIVLWDNRSHRRTPVQRTPLSAAAHTHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
NP_004402.1(human)	361	YSGQIVLWDNRSHRRTPVQRTPLSAAAHTHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
NP_062107.1(rat)	359	YSGQIVLWDNRSHRRTPVQRTPLSAAAHTHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
Consensus	358	YSGQIVLWDNRSHRRTPVQRTPLSAAAHTHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
NP_034193.1(mouse)	404	DMLSTPQESMELVYNKSKFPVAVTGMAFFTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_004402.1(human)	421	DMLSTPQESMELVYNKSKFPVAVTGMAFFTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_062107.1(rat)	419	DMLSTPQESMELVYNKSKFPVAVTGMAFFTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
Consensus	418	DMLSTPQESMELVYNKSKFPVAVTGMAFFTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_034193.1(mouse)	464	EGHQGPVTGINCHMAVGPIDFSHLFVTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMW
NP_004402.1(human)	481	EGHQGPVTGINCHMAVGPIDFSHLFVTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMW
NP_062107.1(rat)	479	EGHQGPVTGINCHMAVGPIDFSHLFVTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMW
Consensus	478	EGHQGPVTGINCHMAVGPIDFSHLFVTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMW

AVAILABLE COPY

(figure 12 continued)

NP_034193.1(mouse)	524	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
NP_004402.1(human)	541	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
NP_062107.1(rat)	539	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
Consensus	538	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
NP_034193.1(mouse)	584	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA
NP_004402.1(human)	601	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA
NP_062107.1(rat)	599	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA
Consensus	598	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA

Amino acid identity: 87%

Amino acid similarity: 88%

The following binding domains are indicated by their N-terminal and C-terminal amino acids (positions correspond to the human amino acid sequence):

p150d (DCTN1 (p150) binding domain)	1M ~ 140E
Tctex1d (Tctex1 binding domain)	157F-174A
10kDad (10kDa light chain binding domain)	164S-174A
2Bd (2B light chain binding domain)	260L-331T

BEST AVAILABLE COPY

## Figure 13. Amino Acid Alignment of Mouse and Human Dynein Intermediate Chain 2 Proteins –Highly Conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

NP_034194.1 (mouse)	1	MSDKS	HLKAELEKRRKQRLAQIREKKRKEERKKKETDQKKEA	VSQVESDLEKKRREA
NP_001369.1 (human)	1	MSDKS	HLKAELEKRRKQRLAQIREKKRKEERKKKETDQKKEA	VAPVQVESDLEKKRREA
Consensus	1	MSDKS	HLKAELEKRRKQRLAQIREKKRKEERKKKETDQKKEA	APVQVESDLEKKRREA
NP_034194.1 (mouse)	61	EALQSMGLT	TSPIV.....	PPPMSPSSKSVSTPSEAGSQDSGDGAVGSF.....
NP_001369.1 (human)	61	EALQSMGLT	TSPIVFSEYVW	PPPMSPSSKSVSTPSEAGSQDSGDGAVGSFTLHWDTDP
Consensus	60	EALQSMGLT	TSPIV.....	PPPMSPSSKSVSTPSEAGSQDSGDGAVGSF.....
NP_034194.1 (mouse)	107	.....	RGPIKLGMAKITQVDFPPREIVTYTKETQTPV	TAQPKDEEEHDDVAT
NP_001369.1 (human)	121	SVLQLHSDSDL	GRGPIKLGMAKITQVDFPPREIVTYTKETQTFVMAQPKDEEEH	DDVVA
Consensus	105	.....	RGPIKLGMAKITQVDFPPREIVTYTKETQTFVMAQPKDEEEH	DDVAA
NP_034194.1 (mouse)	155	PKPPPEPEE	ETLKKDEENDSKAPPHELTEEEKQQILHSEEF	LSFFDHSTRIVERALSEQ
NP_001369.1 (human)	181	PKPPPEPEE	ETLKKDEENDSKAPPHELTEEEKQQILHSEEF	LSFFDHSTRIVERALSEQ
Consensus	152	PKPPPEPEE	ETLKKDEENDSKAPPHELTEEEKQQILHSEEF	LSFFDHSTRIVERALSEQ
NP_034194.1 (mouse)	215	INIFFDYSGRD	LEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	
NP_001369.1 (human)	241	INIFFDYSGRD	LEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	
Consensus	211	INIFFDYSGRD	LEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	
NP_034194.1 (mouse)	275	NNEEAPHEPD	GVALVNMKYKTTPEYVFHCQSAVMSATFAKFHFNLVVGGTYSQQIVLW	
NP_001369.1 (human)	301	NNEEAPHEPD	GVALVNMKYKTTPEYVFHCQSAVMSATFAKFHFNLVVGGTYSQQIVLW	
Consensus	271	NNEEAPHEPD	GVALVNMKYKTTPEYVFHCQSAVMSATFAKFHFNLVVGGTYSQQIVLW	
NP_034194.1 (mouse)	335	DNRSNKRTPV	QRTPLSAAAHTHPVYCVNVVGTQNAHNLSISTDGKICSWSLDMLSHPQD	
NP_001369.1 (human)	361	DNRSNKRTPV	QRTPLSAAAHTHPVYCVNVVGTQNAHNLSISTDGKICSWSLDMLSHPQD	
Consensus	330	DNRSNKRTPV	QRTPLSAAAHTHPVYCVNVVGTQNAHNLSISTDGKICSWSLDMLSHPQD	
NP_034194.1 (mouse)	395	SMELVHKQSK	AVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	
NP_001369.1 (human)	421	SMELVHKQSK	AVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	
Consensus	390	SMELVHKQSK	AVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	
NP_034194.1 (mouse)	455	GIHCHAAVGA	VDVFSHLFVTSSFDWTVKLWTTKNNKPLYSFEDN	ADYVDVVMWSPTHALF
NP_001369.1 (human)	481	GIHCHAAVGA	VDVFSHLFVTSSFDWTVKLWTTKNNKPLYSFEDN	ADYVDVVMWSPTHALF
Consensus	450	GIHCHAAVGA	VDVFSHLFVTSSFDWTVKLWTTKNNKPLYSFEDN	ADYVDVVMWSPTHALF
NP_034194.1 (mouse)	515	ACVDGMGRDL	WNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSEGOQIVYDVG	
NP_001369.1 (human)	541	ACVDGMGRDL	WNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSEGOQIVYDVG	
Consensus	510	ACVDGMGRDL	WNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSEGOQIVYDVG	
NP_034194.1 (mouse)	575	EQIAVPRNDE	WARFGRTLAEINANRADAEEEAATRI	PA
NP_001369.1 (human)	601	EQIAVPRNDE	WARFGRTLAEINANRADAEEEAATRI	PA
Consensus	570	EQIAVPRNDE	WARFGRTLAEINANRADAEEEAATRI	PA

Amino acid identity: 94%  
Amino acid similarity: 95%

BEST AVAILABLE COPY

## Figure 14. Amino Acid Alignment of Mouse, Rattus Norvegicus, and Human Dynein Intermediate Chain 2 Proteins –Highly Conserved Amino Acid Residues.

Software used:

MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

		<b>1M</b>
NP_034194.1(mouse)	1	MSDKS[ <b>L</b> ]KAELEKKQRLAQIREKKRKEEERKKKETDQKKEAAVSVQEEEDLEKKRREA
NP_001369.1(human)	1	MSDKSELKAELEKKQRLAQIREKKRKEEERKKKETDQKKEA <b>V</b> APVQEEEDLEKKRREA
NP_446332.1(rat)	1	MSDKSELKAELEKKQRLAQIREKKRKEEERKKKETDQKKEAAVSVQEEEDLEKKRREA
Consensus	1	MSDKS[ <b>L</b> ]KAELEKKQRLAQIREKKRKEEERKKKETDQKKEAAVSVQEEEDLEKKRREA
NP_034194.1(mouse)	61	EALLQSMGLTTDSPIV.....PPPMSPSSKSVSTPSEAGSQDSGDGAVGSF.....
NP_001369.1(human)	61	EALLQSMGLTTDSPIVFSEYVPPPMSPSSKSVSTPSEAGSQDSGDGAVGSRTLHWDTDF
NP_446332.1(rat)	61	EALLQSMGLTTDSPIVFSEYVPPPMSPSSKSVSTPSEAGSQDSGDGAVGSRTLHWDTDF
Consensus	60	EALLQSMGLTTDSPIVFSEYVPPPMSPSSKSVSTPSEAGSQDSGDGAVGSRTLHWDTDF
		<b>148F 149P 155T 165M</b>
NP_034194.1(mouse)	107	.....SGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAT
NP_001369.1(human)	121	SVLQLHSDSDLCRGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAA
NP_446332.1(rat)	121	SVLQLHSDSDLCRGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAA
Consensus	118	S.LQLHSDSDLCRGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAA
NP_034194.1(mouse)	155	PKPPVEPEEEKTLKKDEENDSKAPPELTHEEKQQILHSEEFLSFFDHSTRIVERALSEQ
NP_001369.1(human)	181	PKPPVEPEEEKTLKKDEENDSKAPPELTHEEKQQILHSEEFLSFFDHSTRIVERALSEQ
NP_446332.1(rat)	181	PKPPVEPEEEKTLKKDEENDSKAPPELTHEEKQQILHSEEFLSFFDHSTRIVERALSEQ
Consensus	176	PKPPVEPEEEKTLKKDEENDSKAPPELTHEEKQQILHSEEFLSFFDHSTRIVERALSEQ
		<b>252L</b>
NP_034194.1(mouse)	215	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN
NP_001369.1(human)	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN
NP_446332.1(rat)	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN
Consensus	235	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN
		<b>323T</b>
NP_034194.1(mouse)	275	NNEEAPHEPDGVALVNMKYKKTTPYVVFHCQSAVMSATFAKFHPNLVVGTYSGQIVLW
NP_001369.1(human)	301	NNEEAPHEPDGVALVNMKYKKTTPYVVFHCQSAVMSATFAKFHPNLVVGTYSGQIVLW
NP_446332.1(rat)	301	NNEEAPHEPDGVALVNMKYKKTTPYVVFHCQSAVMSATFAKFHPNLVVGTYSGQIVLW
Consensus	295	NNEEAPHEPDGVALVNMKYKKTTPYVVFHCQSAVMSATFAKFHPNLVVGTYSGQIVLW
NP_034194.1(mouse)	335	DNRSNKRTPVQRTPLSAAAHTEPVYCVNVVGTQNAHNLISISTDGKICSWSLDMLSHPDQ
NP_001369.1(human)	361	DNRSNKRTPVQRTPLSAAAHTEPVYCVNVVGTQNAHNLISISTDGKICSWSLDMLSHPDQ
NP_446332.1(rat)	361	DNRSNKRTPVQRTPLSAAAHTEPVYCVNVVGTQNAHNLISISTDGKICSWSLDMLSHPDQ
Consensus	354	DNRSNKRTPVQRTPLSAAAHTEPVYCVNVVGTQNAHNLISISTDGKICSWSLDMLSHPDQ
NP_034194.1(mouse)	395	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
NP_001369.1(human)	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
NP_446332.1(rat)	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
Consensus	414	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
NP_034194.1(mouse)	455	GIHCHAAVGAVDFSHLFVTSSFDWTIVKLWTTKNNKPLYSFEDNSDYVYDVVMSPTHPALF
NP_001369.1(human)	481	GIHCHAAVGAVDFSHLFVTSSFDWTIVKLWTTKNNKPLYSFEDNSDYVYDVVMSPTHPALF
NP_446332.1(rat)	481	GIHCHAAVGAVDFSHLFVTSSFDWTIVKLWTTKNNKPLYSFEDNSDYVYDVVMSPTHPALF
Consensus	474	GIHCHAAVGAVDFSHLFVTSSFDWTIVKLWTTKNNKPLYSFEDNSDYVYDVVMSPTHPALF
NP_034194.1(mouse)	515	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSSEGQIVYIDVG
NP_001369.1(human)	541	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSSEGQIVYIDVG
NP_446332.1(rat)	541	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSSEGQIVYIDVG
Consensus	534	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDSSEGQIVYIDVG

BEST AVAILABLE COPY



(Figure 13 continued)

NP_034194.1 (mouse)	575	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIPA
NP_001369.1 (human)	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIPA
NP_446332.1 (rat)	601	EQIAVPRNDEWARFGRTLAEINASRADAEEEEATRIPA
Consensus	594	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIF

Amino acid identity: 93,5%

Amino acid similarity: 94,5%

The following binding domains are indicated (positions correspond to the human amino acid sequence):

P150d (DCTN1 (p150) binding domain)	1M-149P
Tctex1d (Tctex1 binding domain)	148F-165T
10kDa (10kda light chain binding domain)	155T-165T
2Bd (2B light chain binding domain)	252L-323T

BEST AVAILABLE COPY

## Figure 15. Amino Acid Alignment of Mouse and Human DCTN1 (p150) Proteins – highly conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

- BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

NP_031861.1(mouse)	1	MAQSRHRHSSRTSPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAIVGATLFATGKWWGV
AAD55811.1 (human)	1	MAQSRHRHYSRTSPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAIVGATLFATGKWWGV
Consensus	1	MAQSRHRHSSRTSPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAIVGATLFATGKWWGV
NP_031861.1(mouse)	61	ILDEAKGKNDGTVOGKRYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
AAD55811.1 (human)	61	ILDEAKGKNDGTVOGKRYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
Consensus	61	ILDEAKGKNDGTVOGKRYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
NP_031861.1(mouse)	121	GADAAAKTSKLRGLKPKFAPTARKTTTRRPKPTRPASTGVAGSSSLGPSGSASAGELSS
AAD55811.1 (human)	121	GADTTAKTSKLRGLKPKFAPTARKTTTRRPKPTRPASTGVAGASSSLGPSGSASAGELSS
Consensus	121	GADAAAKTSKLRGLKPKFAPTARKTTTRRPKPTRPASTGVAGASSSLGPSGSASAGELSS
NP_031861.1(mouse)	181	SEPSTPAQTPLAAPIIPTPALTSPGAAPPLPSPSKEEGLRAQVRDLEEKLETIRLKRSE
AAD55811.1 (human)	181	SEPSTPAQTPLAAPIIPTPALTSPGAAPPLPSPSKEEGLRAQVRDLEEKLETIRLKRSE
Consensus	181	SEPSTPAQTPLAAPIIPTPALTSPGAAPPLPSPSKEEGLRAQVRDLEEKLETIRLKRSE
NP_031861.1(mouse)	241	DKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
AAD55811.1 (human)	241	DKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
Consensus	241	DKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
NP_031861.1(mouse)	301	ADAIEMATLDKEMAEERAESLQOEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
AAD55811.1 (human)	301	ADAIEMATLDKEMAEERAESLQOEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
Consensus	301	ADAIEMATLDKEMAEERAESLQOEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
NP_031861.1(mouse)	361	KQLEEQNARLKDALVPMRDLSSEKQEHVKLQKLMEKKNQLEVVRRQRRERLQEELSQA
AAD55811.1 (human)	361	KQLEEQNARLKDALVPMRDLSSEKQEHVKLQKLMEKKNQLEVVRRQRRERLQEELSQA
Consensus	361	KQLEEQNARLKDALVPMRDLSSEKQEHVKLQKLMEKKNQLEVVRRQRRERLQEELSQA
NP_031861.1(mouse)	421	STIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDLQENARE
AAD55811.1 (human)	421	STIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDLQENARE
Consensus	421	STIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDLQENARE
NP_031861.1(mouse)	481	TELELREQLDNAGARVREAQRVEAAQETVADYQOTIKKYRQLTAHLQDVNRELTNQOE
AAD55811.1 (human)	481	TELELREQLDNAGARVREAQRVEAAQETVADYQOTIKKYRQLTAHLQDVNRELTNQOE
Consensus	481	TELELREQLDNAGARVREAQRVEAAQETVADYQOTIKKYRQLTAHLQDVNRELTNQOE
NP_031861.1(mouse)	541	SVERQQQPPPETFDFFIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
AAD55811.1 (human)	541	SVERQQQPPPETFDFFIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
Consensus	541	SVERQQQPPPETFDFFIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
NP_031861.1(mouse)	601	GDHDCVLVLLMPRLICFAELIRKQAQEKFLSENCSERPGLRGAAGEQLSFAAGLVYSI
AAD55811.1 (human)	601	GDHDCVLVLLMPRLICFAELIRKQAQEKFLSENCSERPGLRGAAGEQLSFAAGLVYSI
Consensus	601	GDHDCVLVLLMPRLICFAELIRKQAQEKFLSENCSERPGLRGAAGEQLSFAAGLVYSI
NP_031861.1(mouse)	661	SLIQATLHRYEHALSQCSVDVYKVGSLYPMSAHERSLDFLIELLHKDQDDETNNVEPL
AAD55811.1 (human)	661	SLIQATLHRYEHALSQCSVDVYKVGSLYPMSAHERSLDFLIELLHKDQDDETNNVEPL
Consensus	660	SLIQATLHRYEHALSQCSVDVYKVGSLYPMSAHERSLDFLIELLHKDQDDETNNVEPL
NP_031861.1(mouse)	721	NKAIKYYQHLYRIHLAEQPEDCTMQLADHIKFTQSALDCMGVEVGRRLRAFLQGGQATDI
AAD55811.1 (human)	721	NKAIKYYQHLYRIHLAEQPEDCTMQLADHIKFTQSALDCMGVEVGRRLRAFLQGGQATDI
Consensus	720	NKAIKYYQHLYRIHLAEQPEDCTMQLADHIKFTQSALDCMGVEVGRRLRAFLQGGQATDI

BEST AVAILABLE COPY

(Figure 15 continued)

NP_031861.1 (mouse)	781	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAALAFGSQVSDTLLDCRKHLTWVVAV
AAD55811.1 (human)	781	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAALAFGQVSDTLLDCRKHLTWVVAV
Consensus	780	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAALAFGQVSDTLLDCRKHLTWVVAV
NP_031861.1 (mouse)	841	LQEVAAAAQLIAPLAENEGLVAALEELAFKASEQIYGSPSSSPYECLRQSCNIIISTM
AAD55811.1 (human)	841	LQEVAAAAQLIAPLAENEGLVAALEELAFKASEQIYGSPSSSPYECLRQSCNIIISTM
Consensus	840	LQEVAAAAQLIAPLAENEGLVAALEELAFKASEQIYGSPSSSPYECLRQSCNIIISTM
NP_031861.1 (mouse)	901	NKLATAMQEGEYDAERPPSKPPVVELRAALRAEITDAEGLGLKLEDRETVIKELKKSLE
AAD55811.1 (human)	901	NKLATAMQEGEYDAERPPSKPPVVELRAALRAEITDAEGLGLKLEDRETVIKELKKSLE
Consensus	900	NKLATAMQEGEYDAERPPSKPPVVELRAALRAEITDAEGLGLKLEDRETVIKELKKSLE
NP_031861.1 (mouse)	961	IKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLDETQALLRKKEFEETMDALC
AAD55811.1 (human)	961	IKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLDETQALLRKKEFEETMDALC
Consensus	960	IKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLDETQALLRKKEFEETMDALC
NP_031861.1 (mouse)	1021	ADIDQLEAEKAEKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQRGAAPGQAPGA
AAD55811.1 (human)	1021	ADIDQLEAEKAEKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQRGAAPGQAPGA
Consensus	1018	ADIDQLEAEKAEKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQRGAAPGQAPGA
NP_031861.1 (mouse)	1081	LPGPGLVKDSPLLLQQISAMRLHISLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
AAD55811.1 (human)	1081	LPGPGLVKDSPLLLQQISAMRLHISLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
Consensus	1078	LPGPGLVKDSPLLLQQISAMRLHISLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
NP_031861.1 (mouse)	1141	GPGGNLVAGALYRKTSQLEKLNQLSTHVVVDITRSSPAAKSFSQAQMEQVAQLKSLSD
AAD55811.1 (human)	1138	GPGSELVAGALYRKTSQLEKLNQLSTHVVVDITRSSPAAKSFSQAQMEQVAQLKSLSD
Consensus	1135	GPGGNLVAGALYRKTSQLEKLNQLSTHVVVDITRSSPAAKSFSQAQMEQVAQLKSLSD
NP_031861.1 (mouse)	1201	TEKLDKDEVLKETVQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
AAD55811.1 (human)	1198	TEKLDKDEVLKETVQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
Consensus	1194	TEKLDKDEVLKETVQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
NP_031861.1 (mouse)	1261	QRHRLVLTQEQLHQLHSRLIS
AAD55811.1 (human)	1258	QRHRLVLTQEQLHQLHSRLIS
Consensus	1253	QRHRLVLTQEQLHQLHSRLIS

Amino acid identity      97%  
Amino acid similarity    98%

BEST AVAILABLE COPY

# Figure 16. Amino Acid Alignment of Mouse, Rattus Norvegicus, and Human DCTN1 (p150) Proteins – highly conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

- BOXSHADE 3.21 via [http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)

		396	
NP_031861.1 (mouse)	1	MAQSKRHMS	SRTPSGSRMSTEASARPLRVGS
NP_077044.1 (rat)	1	MAQSKRHMYN	RTPSGSRMSTEASARPLRVGS
AAD55811.1 (human)	1	MAQSKRHY	YSRTPSGSRMS
Consensus	1	MAQSKRHMS	SRTPSGSRMSTEASARPLRVGS
		133G 150P	
NP_031861.1	61	ILDEAKGNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
NP_077044.1	61	ILDEAKGNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
AAD55811.1	61	ILDEAKGNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
Consensus	61	ILDEAKGNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
NP_031861.1	121	GADAAAKTSKLRGL	PKKAPTARKTTTRRPKPTRPASTGVAGPSSSLGPSGSASAGELSS
NP_077044.1	121	GADAAAKTSKLRGL	PKKAPTARKTTTRRPKPTRPASTGVAGPSSSLGPSGSASAGELSS
AAD55811.1	121	GADAAAKTSKLRGL	PKKAPTARKTTTRRPKPTRPASTGVAGPSSSLGPSGSASAGELSS
Consensus	120	GADAAAKTSKLRGL	PKKAPTARKTTTRRPKPTRPASTGVAGPSSSLGPSGSASAGELSS
NP_031861.1	181	SEPSTPAQTPLAAPI	IPTPALTSFGAAPPPLSPSKEEEGLRAQVRDLEEKLETLRKRSE
NP_077044.1	181	SEPSTPAQTPLAAPI	IPTPALTSFGAAPPPLSPSKEEEGLRAQVRDLEEKLETLRKRSE
AAD55811.1	181	SEPSTPAQTPLAAPI	IPTPALTSFGAAPPPLSPSKEEEGLRAQVRDLEEKLETLRKRSE
Consensus	180	SEPSTPAQTPLAAPI	IPTPALTSFGAAPPPLSPSKEEEGLRAQVRDLEEKLETLRKRSE
NP_031861.1	241	DKAKLKELEKHKI	QLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
NP_077044.1	241	DKAKLKELEKHKI	QLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
AAD55811.1	241	DKAKLKELEKHKI	QLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
Consensus	240	DKAKLKELEKHKI	QLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYMEEMADT
NP_031861.1	301	ADAIEMATLDKEMAE	ERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
NP_077044.1	300	ADAIEMATLDKEMAE	ERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
AAD55811.1	301	ADAIEMATLDKEMAE	ERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
Consensus	300	ADAIEMATLDKEMAE	ERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
NP_031861.1	361	KQLEEQNARLKDAL	VPMRDLSSSEKQEHVKLQKLMEKKNQLELVVRQQRERLQEELSQA
NP_077044.1	360	KQLEEQNARLKDAL	VPMRDLSSSEKQEHVKLQKLMEKKNQLELVVRQQRERLQEELSQA
AAD55811.1	361	KQLEEQNARLKDAL	VPMRDLSSSEKQEHVKLQKLMEKKNQLELVVRQQRERLQEELSQA
Consensus	360	KQLEEQNARLKDAL	VPMRDLSSSEKQEHVKLQKLMEKKNQLELVVRQQRERLQEELSQA
NP_031861.1	421	STIDELKEQVDAAL	GAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDELQENARE
NP_077044.1	420	STIDELKEQVDAAL	GAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDELQENARE
AAD55811.1	421	STIDELKEQVDAAL	GAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDELQENARE
Consensus	420	STIDELKEQVDAAL	GAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDELQENARE
NP_031861.1	481	TELELREQLDMAGAR	VPEAQKRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
NP_077044.1	480	TELELREQLDMAGAR	VPEAQKRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
AAD55811.1	481	TELELREQLDMAGAR	VPEAQKRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
Consensus	480	TELELREQLDMAGAR	VPEAQKRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
NP_031861.1	541	SVERQQQPPPET	FDFAIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPDSFLRPG
NP_077044.1	540	SVERQQQPPPET	FDFAIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPDSFLRPG
AAD55811.1	541	SVERQQQPPPET	FDFAIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPDSFLRPG
Consensus	540	SVERQQQPPPET	FDFAIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPDSFLRPG
NP_031861.1	601	GDHDCVLVLLMPRL	ICKAELIRKQAEKFDLSENC SERPGLRGAAGEQLSFAAGLVYS
NP_077044.1	600	GDHDCVLVLLMPRL	ICKAELIRKQAEKFDLSENC SERPGLRGAAGEQLSFAAGLVYS
AAD55811.1	601	GDHDCVLVLLMPRL	ICKAELIRKQAEKFDLSENC SERPGLRGAAGEQLSFAAGLVYS
Consensus	600	GDHDCVLVLLMPRL	ICKAELIRKQAEKFDLSENC SERPGLRGAAGEQLSFAAGLVYS

BEST AVAILABLE COPY

(Figure 16 continued)

NP_031861.1	661	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
NP_077044.1	660	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
AAD55811.1	661	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
Consensus	659	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
NP_031861.1	721	NKGIKYQHLYSIHLAEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
NP_077044.1	720	TKAIKYQHLYSIHLAEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
AAD55811.1 (human)	721	TKAIKYQHLYSIHLAEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
Consensus	719	TKAIKYQHLYSIHLAEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
NP_031861.1	781	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
NP_077044.1	780	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
AAD55811.1 (human)	781	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
Consensus	778	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
NP_031861.1	841	LOEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
NP_077044.1	840	LOEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
AAD55811.1 (human)	841	LOEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
Consensus	838	LOEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
NP_031861.1	901	NKLATAMQEGEYDAERPPSKPPVPELRAAALRAEITDAEGLGLKLEDRETVIKELKKSLE
NP_077044.1	900	NKLATAMQEGEYDAERPPSKPPVPELRAAALRAEITDAEGLGLKLEDRETVIKELKKSLE
AAD55811.1 (human)	901	NKLATAMQEGEYDAERPPSKPPVPELRAAALRAEITDAEGLGLKLEDRETVIKELKKSLE
Consensus	897	NKLATAMQEGEYDAERPPSKPPVPELRAAALRAEITDAEGLGLKLEDRETVIKELKKSLE
NP_031861.1	961	IKGEELSEANVRLSLEKKLDSAADADDERIEKVQTRLEETQTLRLKKEKEFEETMDALQ
NP_077044.1	960	IKGEELSEANVRLSLEKKLDSAADADDERIEKVQTRLEETQTLRLKKEKEFEETMDALQ
AAD55811.1 (human)	961	IKGEELSEANVRLSLEKKLDSAADADDERIEKVQTRLEETQTLRLKKEKEFEETMDALQ
Consensus	957	IKGEELSEANVRLSLEKKLDSAADADDERIEKVQTRLEETQTLRLKKEKEFEETMDALQ
NP_031861.1	1021	ADIDQLEAEKRAELKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGIPGOAPGA
NP_077044.1	1020	ADIDQLEAEKRAELKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGIPGOAPGA
AAD55811.1 (human)	1021	ADIDQLEAEKRAELKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGIPGOAPGA
Consensus	1015	ADIDQLEAEKRAELKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGIPGOAPGA
NP_031861.1	1081	LPGPGLVKDSPLLQQISAMRLHISQLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
NP_077044.1	1080	LPGPGLVKDSPLLQQISAMRLHISQLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
AAD55811.1 (human)	1081	LPGPGLVKDSPLLQQISAMRLHISQLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
Consensus	1074	LPGPGLVKDSPLLQQISAMRLHISQLOHENSILRGAQMKASLAALPPLHVAKLSLPPHE
NP_031861.1	1141	GPGGNLMAGALYRKTSQLEKLNQLSTHTHVVDITRSPPAKSPSAQLMEQVAQLKSLSD
NP_077044.1	1140	GPGGNLMAGALYRKTSQLEKLNQLSTHTHVVDITRSPPAKSPSAQLMEQVAQLKSLSD
AAD55811.1 (human)	1138	GPGGNLMAGALYRKTSQLEKLNQLSTHTHVVDITRSPPAKSPSAQLMEQVAQLKSLSD
Consensus	1134	GPGGNLMAGALYRKTSQLEKLNQLSTHTHVVDITRSPPAKSPSAQLMEQVAQLKSLSD
NP_031861.1	1201	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
NP_077044.1	1200	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
AAD55811.1 (human)	1198	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
Consensus	1192	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
NP_031861.1	1261	QRRLVLTQEQQLHQLHSRLIS
NP_077044.1	1260	QRRLVLTQEQQLHQLHSRLIS
AAD55811.1 (human)	1258	QRRLVLTQEQQLHQLHSRLIS
Consensus	1251	QRRLVLTQEQQLHQLHSRLIS

Amino acid identity: 95%

Amino acid similarity: 96%

The following binding domains are indicated by their N-terminal and C-terminal amino acid (positions correspond to the human amino acid sequence):

Microd (microtubules binding domain)	39G – 150P
Dict (dynein intermediate chain1 binding domain)	133G-899T
ARP1d (ARP1 binding domain)	1006R-1021A

BEST AVAILABLE COPY